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82382

From: Schmidt, Mary
Sent: Sunday, December 15, 2002 5:40 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request 09/121,239

Please search the following primer sequences, and please size limit the results to less than 100 bases:

SEQ ID NOS: 1, 5, 9, 13, 16, 22, 23, 26 and 27.

Thanks,
Melissa
mailboxes 11e12
art unit 1635

Priority July 23, 1997
(Prov.)

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
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Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

XX 23-JUL-1999, 99WO-US16832.
PE
XX
XX 23-JUL-1998, 98US-012139.
PR
XX
XX (GENP-) GEN-PROBE INC.
PA
XX
XX Harvey RC, Eastman PS;
PI
XX
XX WPI; 2000-182730/16.
DR
XX
XX Novel methods for preparing RNA from biological samples, used for the
PT

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associated with cancers,
CC particularly forms of leukemia.

XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 other;

Query Match 100.0%; Score 54; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCCTATATAGGAGACTGACCTGAGGCTCAAGTCAGA 54
DB 54 TAAATTAAATACGACTCCTATATAGGAGACTGACCTGAGGCTCAAGTCAGA 1

RESULT 4

ID AAZ60843 standard; RNA; 54 BP.

XX AAZ60843;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KM clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

XX (GENP-) GEN-PROBE INC.

PA Harvey RC, Eastman PS;

PI WPI; 2000-182730/46.

PT Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids
PS Claim 19; Page 40; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associated with cancers,
CC particularly forms of leukemia.

XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 other;

Query Match 100.0%; Score 54; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCCTATATAGGAGACTGACCTGAGGCTCAAGTCAGA 54
DB 54 TAAATTAAATACGACTCCTATATAGGAGACTGACCTGAGGCTCAAGTCAGA 1

RESULT 5

ID AA086626 standard; DNA; 50 BP.

XX AA086626;

DT 15-NOV-1995 (first entry)

DE CML chromosomal translocation minus strand primer.

XX Primer; autocatalytic; target; CML; translocation; ss.

OS Synthetic.

PN US5399491-A.

PD 21-MAR-1995.

PF 11-JUL-1989; 89US-0379501.

PR 11-JUL-1989; 89US-0379501.

PR 10-JUL-1990; 90US-0550837.

PR 19-MAR-1992; 92US-0855732.

XX (GENP-) GEN-PROBE INC.

PA Fultz TJ, Kacian DL;

PI WPI; 1995-130686/17.

PT Amplification of nucleic acid targets - using a reverse
PT transcriptase with RNase H activity and a RNA polymerase at
PT constant temp.

PS Disclosure; Column 9; 58pp; English.

CC AA086626-28 are primers and a probe for the CML chromosomal;
CC translocation. They are used to produce autocatalytic
CC oligonucleotides which require no change in the experimental
CC conditions i.e. constant temperature, pH and ionic strength.
CC These sequences are useful in generating multiple copies of
CC specific nucleic acid target sequences.

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 90.7%; Score 49; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCCTATATAGGAGACTGACCTGAGGCTCAAGTCAGA 51
DB 2 AATTAATACGACTCCTATATAGGAGACTGACCTGAGGCTCAAGTCAGA 50

RESULT 6

AA142417

44 9.2820

ID AAT42417 standard; DNA: 50 BP.
 XX
 AC AAT42417;
 XX
 DT 28-APR-1997 (first entry)
 XX
 DE CML chromosomal translocation primer #1.
 XX
 KM HIV; probe; primer; amplify; polymerase chain reaction; microorganism;
 KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
 XX
 OS Synthetic.
 OS
 PN EP731175-A2.
 XX
 PD 11-SEP-1996.
 XX
 PF 10-JUL-1990; 90EP-0307503.
 XX
 PR 11-JUL-1989; 89US-0379501.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI McDonough S;
 XX
 DR WPI; 1996-403995/41.
 XX
 PT Detection of HIV nucleic acids in samples - using new specific
 PT oligo-nucleotide(s) for the amplification and detection of target
 PT sequences.
 XX
 PS Disclosure; Page 8; 66pp; English.
 XX
 CC AAT42417-T42419 represent primers and a probe for the CML chromosomal
 CC translocation t(9;22). These sequences can be used in modified versions
 CC of the kits of the invention. The kits of the invention, are for
 CC detecting the presence of HIV nucleic acid sequences in a sample. The
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),
 CC and a probe (such as AAT42404) for detection of the amplified sequence.
 CC By using these sequences, the amplification of HIV nucleic acid sequences
 CC is improved. The kits can also be used for the detection of other
 CC microorganisms, by using different probe sequences. Other sequences
 CC that can be detected using this method include those from HBV (using the
 CC sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42416).
 CC The samples can be clinical, environmental or forensic samples, and the
 CC method produces large amounts of the target sequence for a variety of
 CC uses. The method can also be used to produce multiple copies of a
 CC target sequence for use in cloning, and sequencing, and to produce probes
 CC for the target sequence.
 XX
 S0 Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 90.7%; Score 49; DB 17; Length 50;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 AATTATACGACTACTATAGGAGACTCAGACCTGAGGCTCAAGTC 51
 |||||||
 DB 2 AATTATACGACTACTATAGGAGACTCAGACCTGAGGCTCAAGTC 50

RESULT 7
 AAT15571
 ID AAT15571 standard; DNA: 50 BP.
 XX
 AC AAT15571;
 XX
 DT 17-JUL-1996 (first entry)
 XX
 DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
 XX
 KW CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
 KW auto-catalytic; synthesis; RNA target sequence; assay; detection;

KM quantification; ss.
 XX
 OS Synthetic.
 XX
 PN US5480784-A.
 XX
 PD 02-JAN-1996.
 XX
 PF 11-JUL-1989; 89US-0379501.
 XX
 PR 10-JUL-1990; 90US-0550837.
 XX
 PR 11-JUL-1989; 89US-0379501.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX
 DR WPI; 1996-068248/07.
 XX
 PT Auto-catalytic synthesis of multiple copies of an RNA target
 PT sequence - uses cooperative action of a DNA and RNA polymerase in
 PT presence of RNase H, useful for detection of target sequence e.g. in
 PT clinical or environmental sample
 XX
 PS Example; Columns 9-10; 51pp; English.
 XX
 CC The present sequence is a primer for the CML-2 chromosomal
 CC translocation major breakpoint t(9;22), which was used to
 CC demonstrate an improved method for synthesizing multiple copies of
 CC a RNA target sequence. The method comprises combining the target
 CC target, a primer which hybridises to the 3'-terminal portion of the
 CC DNA primer extension prod., reverse transcriptase, RNase H and
 CC and/or quantitate specific target sequences in clinical
 CC environmental or forensic samples. It also has the advantages of
 CC being autocatalytic, using the cooperative action of a DNA
 CC polymerase, e.g. a reverse transcriptase and avoids repetitive
 CC manipulations of reaction conditions, e.g. temp., ionic strength
 CC and pH.
 XX
 S0 Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 90.7%; Score 49; DB 17; Length 50;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 AATTATACGACTACTATAGGAGACTCAGACCTGAGGCTCAAGTC 51
 |||||||
 DB 2 AATTATACGACTACTATAGGAGACTCAGACCTGAGGCTCAAGTC 50

RESULT 8
 AAV66349
 ID AAV66349 standard; DNA: 50 BP.
 XX
 AC AAV66349;
 XX
 DT 06-JAN-1999 (first entry)
 XX
 DE CML-2 chromosomal translocation t(9;22) primer.
 XX
 KW CML-2 chromosomal translocation t(9;22); block splice template;
 KW autocatalytic RNA amplification; primer; ss.
 XX
 OS Synthetic.
 OS
 PN US5824518-A.
 XX
 PD 20-OCT-1998.
 XX
 PF 06-JUN-1995; 95US-0469067.

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PR 10-JUL-1990; 90US-0550837.
PR 11-JUL-1989; 89US-0379501.
PR 06-JUN-1995; 95US-0469067.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Fulz TJ, Kacian DL;
XX
XX WPI: 1998-582557/49.
XX
XX Block splice template useful for amplification of nucleic acids -
XX comprises two nucleic acid regions: the first region located 3' of
XX the second region and blocked at its 3' terminus to inhibit primer
XX extension by a DNA polymerase
XX
XX Example 15; Column 9; 51pp; English.
XX
XX AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,
XX for the (+) and (-) strands respectively. The primers are used to
XX exemplify the invention, together with probe AAV6351. The specification
XX describes methods of synthesizing multiple copies of a target nucleic
XX acid sequence autocatalytically under conditions of substantially
XX constant temperature, ionic strength and pH are provided in which
XX multiple RNA copies of the target sequence autocatalytically
XX generate additional copies. The target sequence is a block splice
XX template which comprises two nucleic acid regions. The first region is
XX located 3' of the second region and is blocked at its 3' terminus to
XX inhibit primer extension by a DNA polymerase, and the second region
XX comprises a promoter sequence recognised by an RNA polymerase. The
XX methods are used to amplify nucleic acids, especially RNA, for
XX analysis, cloning or probe production.
XX
XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other:
XX
XX Query Match 90.7%; Score 49; DB 19; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-10;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 AATTAAATCGACTCTATATAGGAGACTGAGACCTGAGGCTCAAAGTC 51
XX |||||||
XX 2 AATTAAATCGACTCTATATAGGAGACTGAGACCTGAGGCTCAAAGTC 50
XX
XX RESULT 9
XX ID AAX23191 standard; DNA: 50 BP.
XX AC AAX23191;
XX XX
XX DT 11-JUN-1999 (first entry)
XX
XX CML chromosomal translocation t(9;22) primer #1.
XX
XX Autocatalytic amplification; transcription-based amplification; CML;
XX thermalcycling; diagnostic; environmental testing; probe; detection;
XX genetic disease; infectious disease; microorganism; food; forensic;
XX paternity; primer; ss.
XX
XX Synthetic.
XX
XX US5888779-A.
XX
XX 30-MAR-1999.
XX
XX 05-JUN-1995; 95US-0461654.
XX
XX 10-JUL-1990; 90US-0550837.
XX 11-JUL-1989; 89US-0379501.
XX 05-JUN-1995; 95US-0461654.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Fulz TJ, Kacian DL;

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XX
XX WPI: 1999-253231/21.
XX
XX Kit for autocatalytic amplification of RNA targets
XX
XX Disclosure; Column 9; 51pp; English.
XX
XX This invention describes a novel method for the autocatalytic
XX amplification of an RNA target in a transcription-based amplification
XX system without thermalcycling. The method generates oligonucleotides for
XX diagnostic or environmental testing, for use e.g. as probes and in
XX cloning. Typical applications are the detection of genetic or infectious
XX diseases, the monitoring of responses to therapy, the quantitation or
XX detection of microorganisms in foods, forensic studies and the
XX establishment of paternity. Kits containing the products of the invention
XX provide many copies of selected RNA targets under conditions of constant
XX temperature, ionic strength and pH. Specific amplification of RNA targets
XX increases sensitivity, convenience, accuracy and the reliability of
XX assays.
XX
XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other:
XX
XX Query Match 90.7%; Score 49; DB 20; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-10;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 AATTAAATCGACTCTATATAGGAGACTGAGACCTGAGGCTCAAAGTC 51
XX |||||||
XX 2 AATTAAATCGACTCTATATAGGAGACTGAGACCTGAGGCTCAAAGTC 50
XX
XX RESULT 10
XX ID AAA76210 standard; DNA: 52 BP.
XX AC AAA76210;
XX XX
XX DT 25-JAN-2001 (first entry)
XX
XX Human prostate specific antigen PCR primer SEQ ID NO: 39.
XX
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200044940-A2.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US02270.
XX
XX 28-JAN-1999; 99US-0117640.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Clark TJ;
XX
XX WPI: 2000-505986/45.
XX
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples
XX using probe molecules, useful for the diagnosis of prostate and breast
XX cancers -
XX
XX Claim 1; Page 13; 77pp; English.
XX
XX The present invention is concerned with the detection of nucleic acid
XX markers for prostate and breast cancer, and PCR primers and probes which
XX are able to detect and quantify these markers. Prostate specific antigen
XX (PSA), prostate-specific membrane antigen (PSMA) and glandular
XX kallikrein-2 (hK2) have all been linked to prostate and breast cancers,

```

CC and the primers and probes of the invention are able to detect the
CC abnormal presence of mRNA expressed by their coding sequences in tissues
CC other than the prostate. This enables the presence of cancer to be
CC perceived and aids in the detection of metastases.

XX
SQ Sequence 52 BP; 18 A; 9 C; 12 G; 13 T; 0 other;

Query Match 59.3%; Score 32; DB 21; Length 52;
Best Local Similarity 79.2%; Pred. No. 0.0021;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TAAATTAATAGCAGCTACTATAGGAGAGACCTGAGGCTCAAA 48
|||||
DB 1 TAAATTAATAGCAGCTACTATAGGAGAGACCTGCTTCAGAGATGAAA 48

RESULT 11
AAA76067
ID AAA76067 standard; DNA; 54 BP.

XX AAA76067;

DT 25-JAN-2001 (first entry)

XX Human prostate specific antigen PCR primer SEQ ID NO: 29.

DE Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
KW glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
XX PCR primer; ss.

OS Homo sapiens.

XX W0200044940-A2.

PD 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US02270.

XX 28-JAN-1999; 99US-0117640.

PA (GENP-) GEN-PROBE INC.

XX Harvey RC, Clark TJ;

DR WPI; 2000-505986/45.

PT Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples
XX using probe molecules, useful for the diagnosis of prostate and breast
XX cancers -

PS Claim 1; Page 12; 77pp; English.

XX The present invention is concerned with the detection of nucleic acid
CC markers for prostate and breast cancer, and PCR primers and probes which
CC are able to detect and quantify these markers. Prostate specific antigen
CC (PSA), prostate-specific membrane antigen (PSMA) and glandular
CC kallikrein-2 (hK2) have all been linked to prostate and breast cancers,
CC and the primers and probes of the invention are able to detect the
CC abnormal presence of mRNA expressed by their coding sequences in tissues
CC other than the prostate. This enables the presence of cancer to be
CC perceived and aids in the detection of metastases.

XX Sequence 54 BP; 16 A; 13 C; 11 G; 14 T; 0 other;

Query Match 59.3%; Score 32; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATAGCAGCTACTATAGGAGAGACTCA 32
|||||
DB 1 TAAATTAATAGCAGCTACTATAGGAGAGACTCA 32

RESULT 12
ABK53140
ID ABK53140 standard; DNA; 51 BP.

XX ABK53140;

DT 12-AUG-2002 (first entry)

XX HIV-1 reverse transcriptase gene specific oligonucleotide primer #11.

DE HIV; human immunodeficiency virus; ss; primer; gag; pol;
KW protease; reverse transcriptase; infection; PCR.

XX Human immunodeficiency virus type 1.

XX US2002055095-A1.

PD 09-MAY-2002.

XX 31-AUG-2001; 2001US-0944036.

XX 01-SEP-2000; 2000US-229790P.

PA (YANG/) YANG Y Y.

PA (BREN/) BRENTANO S T.

PA (BARO/) BAROLA O.

PA (TRAN/) TRAN N.

XX (VERN/) VERNET G.

XX Yang YY, Brentano ST, Barola O, Tran N, Vernet G;

XX WPI; 2002-462902/49.

PS Claim 1; Page 25; 37pp; English.

XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridises to an HIV-1 sequence
CC derived from gag or pol sequences, having one of the sequences fully
CC defined in the specification, and a method for detecting HIV-1 in a
CC biological sample, comprising mixing the sample with two or more of the
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The present sequence represents a PCR
CC primer used to amplify the HIV-1 reverse transcriptase gene in the HIV
CC detection method of the invention.

XX Sequence 51 BP; 17 A; 11 C; 8 G; 15 T; 0 other;

Query Match 58.9%; Score 31.8; DB 24; Length 51;
Best Local Similarity 76.5%; Pred. No. 0.0025;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 AAATTAATAGCAGCTACTATAGGAGAGACTGAGGCTCAAGTCA 52
|||||
DB 1 AAATTAATAGCAGCTACTATAGGAGAGACTGAGGCTCAAGTCA 51

RESULT 13

XX AAL45502
ID AAL45502 standard; DNA; 51 BP.

XX AAL45502;

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 ; Search time 82.3837 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-5

Sequence: 1 GACCACTGCTGTGTAACCTCA 24

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	24	16	AA086635	Modified non-prom
2	24	100.0	24	19	AAV66353	CML-2 chromosomal
3	24	100.0	24	20	AAV63985	bcr-abl sense prim
4	24	100.0	24	20	AAV63204	CML t(14; 18) non-
5	24	100.0	24	21	AAV60844	oligonucleotide us
6	24	100.0	24	21	AAV60845	oligonucleotide us
7	24	100.0	24	21	AAV60846	oligonucleotide us
8	24	100.0	24	21	AAV60847	oligonucleotide us
9	21	87.5	40	15	AA066789	L6 bcr exon 2/abl

10	20	83.3	20	14	AA051829	bcr mRNA ribozyme
11	19	79.2	47	18	AAV91751	Primer BB326 for b
12	17	70.8	47	18	AAV91749	Primer BB232 for b
13	16	66.7	22	24	AB092608	Human leukemia ch
14	16	66.7	40	19	AAV58775	Forward primer for
15	15	62.5	47	17	AAV03636	3SR primer 325. S
16	15	62.5	47	18	AAV03636	Primer BB325 for b
17	15	62.5	51	21	AAV76855	Human clone c93940
18	14.6	60.8	51	22	AAV29108	Human SNP oligonuc
19	14.4	60.0	20	20	AAV97409	Primer used to amp
20	14.4	60.0	60	24	ABN34009	Human spliced tran
21	14.4	60.0	60	24	ABN56313	Mouse spliced tran
22	14	58.3	33	17	AAV31737	Escherichia coli t
23	14	58.3	38	20	AAV84137	PCR primer for Ara
24	14	58.3	60	24	ABN33510	Human spliced tran
25	14	58.3	60	24	ABN36796	Human spliced tran
26	14	58.3	65	24	ABN53882	Mouse spliced tran
27	14	58.3	65	24	ABN54134	Mouse spliced tran
28	13.8	57.5	60	24	ABN31655	Human spliced tran
29	13.8	57.5	60	24	ABN44873	Downstream sequenc
30	13.8	57.5	76	13	AA033613	Flaviviral hybrid
31	13.6	56.7	28	16	AA080792	Rat galanin recept
32	13.6	56.7	46	23	AA035843	Human ERG amberzy
33	13.6	56.7	48	23	AAK07037	Human ERG amberzy
34	13.6	56.7	51	22	AAK21959	Human ERG amberzy
35	13.6	56.7	60	24	ABN45501	Human spliced tran
36	13.6	56.7	60	24	ABN45501	Human spliced tran
37	13.6	56.7	60	24	ABN30666	Rat spliced trans
38	13.6	56.7	65	21	AAV14815	DNA encoding a wil
39	13.6	56.7	69	21	AAV14815	Primer for chicken
40	13.4	55.8	51	21	AAV88367	Human clone c93940
41	13.4	55.8	60	24	ABN58935	Human spliced tran
42	13.4	55.8	60	24	AAV30013	Oligonucleotide IF
43	13.4	55.8	80	20	AAV30014	Oligonucleotide IF
44	13.4	55.8	80	20	AAV30014	Oligonucleotide us
45	13.4	55.8	80	20	AAV35329	Oligonucleotide us

ALIGNMENTS

AA086635	standard; DNA; 24 BP.
AA086635	16-NOV-1995 (first entry)
AA086635	Modified non-promoter primer for the CML major breakpoint region.
AA086635	Primer; autocatalytic; PCR; target; sequence; ss.
AA086635	Synthetic.
US5399491-A.	
21-MAR-1995.	
11-JUL-1989.	89US-0379501.
11-JUL-1989.	89US-0379501.
10-JUL-1990.	90US-0550837.
19-MAR-1992.	92US-0855732.
(GENP-) GEN-PROBE INC.	
Fultz TJ, Kacian DL;	
WPI; 1995-130686/17.	
Amplification of nucleic acid targets - using a reverse	
transcriptase with RNase H activity and a RNA polymerase at	

PT constant temp.
 XX
 PS Example 18; Column 47; 58pp; English.
 CC
 CC The oligonucleotide AA086635 is a non-promoter primer for the CML
 CC major breakpoint amplification region. It is used to illustrate
 CC that small changes in the NA sequence result in large changes in
 CC the amplification efficiency. AA086635 is capable of serving as a
 CC primer for the synthesis of autocatalytic oligonucleotides which
 CC require no change in the PCR conditions i.e. constant temperature,
 CC pH and ionic strength. This sequence is useful in generating
 CC multiple copies of specific nucleic acid target sequences.
 SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
 QY
 Query Match 100.0%; Score 24; DB 16; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 GACCAACTGCTGTGTGAACCTCA 24
 1 GACCAACTGCTGTGTGAACCTCA 24
 RESULT 2
 AAV66353
 ID AAV66353 standard; DNA; 24 BP.
 XX
 AC AAV66353;
 XX
 DT 06-JAN-1999 (first entry)
 DE CML-2 chromosomal translocation major breakpoint non-promoter primer.
 XX
 KM CML-2 chromosomal translocation t(14;18) major breakpoint;
 KM block splice template; autocatalytic RNA amplification; primer; ss.
 XX
 OS Synthetic.
 OS
 XX US5824518-A.
 PN 20-0CT-1998.
 PD 06-JUN-1995; 95US-0469067.
 PF 10-JUL-1990; 90US-0550837.
 PR 11-JUL-1989; 89US-0379501.
 PR 06-JUN-1995; 95US-0469067.
 XX
 XX (GENP-) GEN-PROBE INC.
 XX
 XX Pultz TJ, Kacian DL;
 XX
 DR WPI; 1998-582557/49.
 XX
 PT Block splice template useful for amplification of nucleic acids -
 PT comprises two nucleic acid regions, the first region located 3' of
 PT the second region and blocked at its 3' terminus to inhibit primer
 PT extension by a DNA polymerase
 XX
 XX Example 18; Column 43; 51pp; English.
 PS
 XX AAV66352-55 represent CML-2 chromosomal translocation t(14;18) major
 CC breakpoint amplification region non-promoter primers. The primers
 CC are used to exemplify the invention. The specification describes
 CC methods of synthesizing multiple copies of a target nucleic acid
 CC sequence autocatalytically under conditions of substantially
 CC constant temperature, ionic strength and pH are provided in which
 CC multiple RNA copies of the target sequence autocatalytically
 CC generate additional copies. The target sequence is a block splice
 CC template which comprises two nucleic acid regions. The first region is
 CC located 3' of the second region and is blocked at its 3' terminus to
 CC inhibit primer extension by a DNA polymerase, and the second region

CC comprises a promoter sequence recognised by an RNA polymerase. The
 CC methods are used to amplify nucleic acids, especially RNA, for
 CC analysis, cloning or probe production.
 CC
 SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
 QY
 Query Match 100.0%; Score 24; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 GACCAACTGCTGTGTGAACCTCA 24
 1 GACCAACTGCTGTGTGAACCTCA 24
 RESULT 3
 AA83985
 ID AA83985 standard; DNA; 24 BP.
 XX
 AC AA83985;
 XX
 DT 08-SEP-1999 (first entry)
 DE bcr-abl sense primer.
 XX
 KM Reverse transcription PCR: oligonucleotide-immobilised microplate;
 KM polypropylene; thermal cycle; solid phase; cell lysate; research;
 KM gene expression analysis; diagnostic; drug screening; primer; ss.
 XX
 OS Synthetic.
 OS
 XX WO9932654-A1.
 PN 01-JUL-1999.
 PD 22-DEC-1998; 98WO-US27293.
 PF 16-JAN-1998; 98US-0071627.
 PR 22-DEC-1997; 97US-0068394.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 XX
 XX Mitsuhashi M;
 XX
 DR WPI; 1999-418942/35.
 XX
 PT Using oligonucleotide-immobilized microplates in polymerase chain
 PT reactions
 XX
 PS Example; Page 9; 34pp; English.
 XX
 CC The present invention describes the use of oligonucleotide-immobilized
 CC microplates having heat-stability for thermal cycles of reverse
 CC transcription-polymerase chain reaction (RT-PCR). The method of RT-PCR
 CC comprises: (a) preparing cell lysate of a target cell; (b) transferring
 CC the cell lysate to an oligonucleotide-immobilized microplate having
 CC wells to which oligonucleotides are securely immobilized, the microplate
 CC having heat-stability for thermal cycles of PCR, the oligonucleotides
 CC having nucleic acid sequences specifically complementary to mRNA of
 CC interest present in the cell lysate; (c) capturing mRNA by the
 CC oligonucleotides of the microplate; (d) conducting RT-PCR on the same
 CC microplate, using an appropriate buffer; and (e) detecting PCR products
 CC of interest. The method is used for gene expression analysis. The
 CC multiple PCR system is useful in basic research, diagnostics and drug
 CC screening, with potential application to future automation. The method
 CC simplifies the process of RT-PCR. cDNA synthesized from mRNA captured by
 CC immobilized oligonucleotide on the PCR microplates can be used more than
 CC once, thus amplifying several times different or same portions of the
 CC cDNA by using appropriate primers. The method also drastically
 CC simplifies the preparation of cell lysate and significantly stabilizes
 CC the yield of recovered cytosolic RNA. The present sequence represents a
 CC primer used in an example from the present invention.


```

XX      Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
SQ      Query Match      100.0%; Score 24; DB 20; Length 24;
      Best Local Similarity 100.0%; Pred. No. 0.022;
      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GACCAACTGCTGTGGAACCTCCA 24
      1 GACCAACTGCTGTGGAACCTCCA 24

DB      1 GACCAACTGCTGTGGAACCTCCA 24

RESULT 4
AAZ3204
ID      AAZ3204 standard; DNA; 24 BP.
AC      AAZ3204;
XX      11-JUN-1999 (first entry)
DT      CML t(14; 18) non-promoter primer #2.
XX      Autocatalytic amplification; transcription-based amplification; CML;
KW      thermal cycling; diagnostic; environmental testing; probe; detection;
KW      genetic disease; infectious disease; microorganism; food; forensic;
KW      paternity; primer; ss.
XX      Synthetic.
XX      US588779-A.
XX      30-MAR-1999.
XX      05-JUN-1995; 95US-0461654.
XX      10-JUL-1990; 90US-0550837.
XX      11-JUL-1989; 89US-0379501.
XX      05-JUN-1995; 95US-0461654.
XX      (GENP-) GEN-PROBE INC.
XX      Fultz TJ, Kacian DL;
XX      WPI: 1999-253231/21.
XX      Kit for autocatalytic amplification of RNA targets
XX      Example 18; Column 43; 51pp; English.
XX      This invention describes a novel method for the autocatalytic
XX      amplification of an RNA target in a transcription-based amplification
XX      system without thermal cycling. The method generates oligonucleotides for
XX      diagnostic or environmental testing, for use e.g., as probes and in
XX      cloning. Typical applications are the detection of genetic or infectious
XX      diseases, the monitoring of responses to therapy, the quantitation or
XX      detection of microorganisms in foods, forensic studies and the
XX      establishment of paternity. Kits containing the products of the invention
XX      provide many copies of selected RNA targets under conditions of constant
XX      temperature, ionic strength and pH. Specific amplification of RNA targets
XX      increases sensitivity, convenience, accuracy and the reliability of
XX      assays.
SQ      Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
XX      Query Match      100.0%; Score 24; DB 20; Length 24;
XX      Best Local Similarity 100.0%; Pred. No. 0.022;
XX      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GACCAACTGCTGTGGAACCTCCA 24
      1 GACCAACTGCTGTGGAACCTCCA 24

DB      1 GACCAACTGCTGTGGAACCTCCA 24

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```

RESULT 5
AAZ60844
ID      AAZ60844 standard; DNA; 24 BP.
AC      AAZ60844;
XX      16-MAY-2000 (first entry)
DT      Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX      DE      Fusion transcript; translocation; bcr b3 region; abl gene;
XX      KW      amplification assay; detection assay; medical diagnosis;
KW      clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW      disease marker; cancer; leukemia; ss.
XX      Synthetic.
XX      WO200005418-A1.
XX      03-FEB-2000.
XX      23-JUL-1999; 99WO-US16832.
XX      23-JUL-1998; 98US-0121239.
XX      (GENP-) GEN-PROBE INC.
XX      Harvey RC, Eastman PS;
XX      WPI: 2000-182730/16.
XX      Novel methods for preparing RNA from biological samples, used for the
XX      detection and measurement of nucleic acids and fusion nucleic acids
XX      Claim 19; Page 40; 49pp; English.
XX      Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX      the invention to detect fusion transcripts produced from a translocation
XX      between the bcr b3 region and the abl gene. The specification describes
XX      a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX      species), in a biological sample. The method comprises contacting a
XX      sample of fusion nucleic acid with primers, amplifying the hybridized
XX      fusion nucleic acid, and detecting the target hybrid. The method is
XX      used for the simple and rapid preparation of RNA from a biological
XX      sample, particularly from the cytoplasm of eukaryotic cells, which is
XX      suitable for use in an amplification and detection assay. The methods
XX      are used for the analysis and detection of nucleic acids in biological
XX      samples. The methods are useful in the human medical and veterinary
XX      fields, for medical diagnoses and clinical monitoring of a patient's
XX      response to therapy where a disease or medical condition is associated
XX      with a particular type and/or level of mRNA present in the sample. The
XX      methods are also useful for detecting or quantifying fusion or chimeric
XX      RNA species, and for detecting a translocation as a marker for a given
XX      condition or disease, e.g., translocations associate with cancers,
XX      particularly forms of leukemia.
SQ      Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
XX      Query Match      100.0%; Score 24; DB 21; Length 24;
XX      Best Local Similarity 100.0%; Pred. No. 0.022;
XX      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GACCAACTGCTGTGGAACCTCCA 24
      1 GACCAACTGCTGTGGAACCTCCA 24

DB      1 GACCAACTGCTGTGGAACCTCCA 24

RESULT 6
AAZ60845
ID      AAZ60845 standard; RNA; 24 BP.
AC      AAZ60845;
XX
XX
XX

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DT 16-MAY-2000 (first entry)
XX
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX
KW Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
OS Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US16832.
XX
XX 23-JUL-1998; 98US-0121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 40; 49pp; English.
XX
XX Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes
XX a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is
XX used for the simple and rapid preparation of RNA from a biological
XX sample, particularly from the cytoplasm of eukaryotic cells, which is
XX suitable for use in an amplification and detection assay. The methods
XX are used for the analysis and detection of nucleic acids in biological
XX samples. The methods are useful in the human medical and veterinary
XX fields, for medical diagnoses and clinical monitoring of a patient's
XX response to therapy where a disease or medical condition is associated
XX with a particular type and/or level of mRNA present in the sample. The
XX methods are also useful for detecting or quantifying fusion or chimeric
XX RNA species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia.
XX
XX Sequence 24 BP; 7 A; 7 C; 5 G; 5 U; 0 other:
XX
XX Query Match 100.0%; Score 24; DB 21; Length 24;
XX Best Local Similarity 79.2%; Pred. No. 0.022;
XX Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 GACCAACTCGTGTGGAACCTCA 24
XX 1 GACCAACUCGUGUGAACAUCCA 24
XX
XX Db 1 GACCAACTCGTGTGGAACCTCA 24
XX 1 GACCAACUCGUGUGAACAUCCA 24
XX
XX RESULT 7
XX AA260846/c
XX ID AA260846 standard; DNA; 24 BP.
XX
XX AC AA260846;
XX
XX 16-MAY-2000 (first entry)
XX
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX
XX

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US16832.
XX
XX 23-JUL-1998; 98US-0121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 40; 49pp; English.
XX
XX Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes
XX a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is
XX used for the simple and rapid preparation of RNA from a biological
XX sample, particularly from the cytoplasm of eukaryotic cells, which is
XX suitable for use in an amplification and detection assay. The methods
XX are used for the analysis and detection of nucleic acids in biological
XX samples. The methods are useful in the human medical and veterinary
XX fields, for medical diagnoses and clinical monitoring of a patient's
XX response to therapy where a disease or medical condition is associated
XX with a particular type and/or level of mRNA present in the sample. The
XX methods are also useful for detecting or quantifying fusion or chimeric
XX RNA species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia.
XX
XX Sequence 24 BP; 5 A; 5 C; 7 G; 7 T; 0 other:
XX
XX Query Match 100.0%; Score 24; DB 21; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 0.022;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 GACCAACTCGTGTGGAACCTCA 24
XX 24 GACCAACTCGTGTGGAACCTCA 1
XX
XX Db 1 GACCAACTCGTGTGGAACCTCA 24
XX 24 GACCAACTCGTGTGGAACCTCA 1
XX
XX RESULT 8
XX AA260847/c
XX ID AA260847 standard; RNA; 24 BP.
XX
XX AC AA260847;
XX
XX 16-MAY-2000 (first entry)
XX
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX

XX 03-FEB-2000.
 PD 23-JUL-1999; 99WO-US16832.
 XX 23-JUL-1998; 98US-0121239.
 PR (GENE-) GEN-PROBE INC.
 PA Harvey RC, Eastman PS;
 XX WPI; 2000-182730/16.
 DR
 XX Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids -
 XX Claim 19, Page 41; 49pp: English.
 XX
 CC Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 CC Sequence 24 BP; 5 A; 5 C; 7 G; 7 U; 0 other;
 SQ
 Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.022; 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0;
 OY 1 GACCACTCGTGTGAACCTCA 24
 DB 24 GACCACTCGTGTGAACCTCA 1
 RESULT 9
 AA066789
 ID AA066789 standard; RNA; 40 BP.
 AC
 AC AA066789;
 DT 10-FEB-1995 (first entry)
 XX
 DE L6 bcr exon 2/abl exon 2 cloning 5' primer.
 XX
 XX Fusion mRNA; L6; hematopoietic cells; chronic myelogenous leukemia;
 KW CML; acute lymphocytic leukemia; ALL; exon 2; abl; bcr; exon 3; K28;
 KW translocation; chromosome 9; chromosome 22; tyrosine kinase; cleavage;
 KW ribozymes; nucleation; anchor sequence; follicular lymphomas; ss.
 XX
 OS Synthetic.
 XX
 XX WO9413793-A.
 XX
 PD 23-JUN-1994.
 XX
 PF 16-NOV-1993; 93WO-US11144.
 XX
 PR 04-DEC-1992; 92US-098652.

XX (APOL-) APOLLON INC.
 PA Coney LR, Oakes FT, Pachuk CJ;
 PI WPI; 1994-217873/26.
 DR
 XX Ribozymes comprising catalytic sequence, two legs and anchor
 PT sequence(s) complementary to substrate mRNA - is used for treatment
 PT of chronic myelogenous leukemia and acute lymphoblastic leukemia
 XX
 XX Disclosure; Page 26; 67pp: English.
 XX
 CC The sequences given in AA066789-95 are primers which were used in the
 CC cloning of fragments of the L6 and K28 fusion mRNAs. These mRNAs are
 CC expressed by some of the hematopoietic cells of some chronic myelogenous
 CC leukemia (CML) and acute lymphocytic leukemia (ALL) patients. In the
 CC L6 mRNA, abl exon 2 is linked to bcr exon 2, and in K28 abl exon 2 is
 CC linked to bcr exon 3. This is caused by a translocation between
 CC chromosomes 9 and 22. The L6 and K28 mRNAs encode a protein with
 CC aberrant tyrosine kinase activity which is unique to CML cells and which
 CC is thought to play a key role in the establishment of CML. The
 CC ribozymes of the invention are specifically targeted to the L6 and K28
 CC mRNAs. Non-contiguous regions of the substrate RNA can be utilized for
 CC the separate events of ribozyme nucleation and ribozyme cleavage. The
 CC ribozymes are targeted to the L6 bcr-abl RNA via an anchor sequence
 CC which is proximal to the bcr-abl junction. Cleavage by these ribozymes
 CC occurs at a downstream site located within an abl specific sequence in
 CC the fusion mRNA. Normal abl and bcr substrates are not cleaved.
 CC Ribozymes such as these are useful in treating diseases involving
 CC translocations eg. CML, ALL and follicular lymphomas. See also
 CC AA066774-96.
 CC
 CC Sequence 40 BP; 12 A; 7 C; 9 G; 12 T; 0 other;
 SQ
 Query Match 87.5%; Score 21; DB 15; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.72; 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;
 OY 4 CAACCTCGTGTGAACCTCA 24
 DB 20 CAACCTCGTGTGAACCTCA 40
 RESULT 10
 AA051829
 ID AA051829 standard; RNA; 20 BP.
 AC
 AC AA051829;
 DT 26-MAY-1994 (first entry)
 XX
 DE bcr mRNA ribozyme cleavable nucleotide 3245.
 XX
 XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
 KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9323057-A.
 XX
 PD 25-NOV-1993.
 XX
 PF 13-MAY-1993; 93WO-US04573.
 XX
 PR 14-MAY-1992; 92US-088282.
 PR 14-MAY-1992; 92US-088285.

PR 26-AUG-1992; 92US-0936110.
 PR 26-AUG-1992; 92US-0936421.
 PR 26-AUG-1992; 92US-0936422.
 PR 26-AUG-1992; 92US-0936531.
 PR 26-AUG-1992; 92US-0936532.
 PR 07-DEC-1992; 92US-0987131.
 PR 19-JAN-1993; 93US-0006122.
 PR 19-JAN-1993; 93US-0008910.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Draper KG, Thompson JD;
 XX
 DR WPI; 1993-386203/48.
 XX
 PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
 PT associated with tumours or mRNA expressed from gene encoding
 PT multiple drug resistance
 XX
 PS Claim 3; Fig 3; 69pp; English.
 XX
 CC The sequences given in A051825-2266 represent areas of mRNAs
 CC associated with development or maintenance of chronic myelogenous
 CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
 CC and lung cancer. The full length mRNAs containing these target
 CC sequences, encode aberrant cellular proteins which are able to control
 CC cellular proliferation and are directly linked to a leukemic
 CC phenotype. These target sequences are identified by the ribozyme of
 CC the invention. The ribozymes is formed in a hammerhead motif, but may
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group
 CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and
 CC other animals by modulating expression of the corresponding gene.
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
 CC cells elicits inhibition of the transformed state. Multiple drug
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
 CC drug resistance used by transformed cells and thus enhances drug
 CC therapies for tumours. The ribozymes may also be used to study
 CC genetic drift and mutations within cells.
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 U; 0 other;
 XX
 Query Match 83.3%; Score 20; DB 14; Length 20;
 Best Local Similarity 75.0%; Pred. No. 2;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 YY 4 CAACCTCGTGTGAACTCC 23
 YY 1 CAACUCGUGUGAACAUC 20
 XX
 RESULT 11
 AAT91751
 ID AAT91751 standard; DNA; 47 BP.
 XX
 AC AAT91751;
 XX
 DT 08-JAN-1998 (first entry)
 XX
 DE Primer BB326 for bcr2-ab12 and bcr3-ab12 translocation regions.
 XX
 KW PCR; primer; amplify; polymerase chain reaction; haematopoietic cell;
 KW chronic myelogenous leukaemia; human; bcr2-ab12; translocation region;
 KW cytogenetic remission; ph chromosome; bcr3-ab12; CML cell;
 KW acute lymphotrophic leukaemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO9708339-A1.
 XX
 PD 06-MAR-1997.

XX
 PE 28-AUG-1995; 95WO-US10919.
 XX
 PR 25-AUG-1995; 95US-0296258.
 XX
 PA (DADE-) DADE INT INC.
 XX
 PI Brown J, Lockhart-bruce C;
 XX
 DR WPI; 1997-179294/16.
 XX
 PT Detection of chronic myelogenous leukemia cells - by amplification
 PT of RNA from haematopoietic cells with primers for the bcr2-ab12 and
 PT bcr3-ab12 trans-location regions
 XX
 PS Claim 3; Page 11; 79pp; English.
 XX
 CC AAT91749-T91763, and AAT91765-T91792 are primers used in the method of
 CC the invention. AAT91754-T91759 can also be used as capture
 CC oligonucleotides (ON), while AAT91760-T91763, AAT91791 and AAT91792 can
 CC also be used as detector agents. The method of the invention is for
 CC detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
 CC human patient. The method comprises obtaining RNA from haematopoietic
 CC cells of the patient, and amplifying it using a pair of primers that
 CC amplify both the bcr2-ab12 and bcr3-ab12 translocation regions. The
 CC amplified sequence is contacted with a capture agent comprising a capture
 CC ON and a binding ligand to form a capture mixture. The capture ON is
 CC specific for the bcr2-ab12 and bcr3-ab12 translocation regions. The
 CC mixture is contacted with a solid phase coupled to a receptor specific
 CC for the binding ligand. The solid phase is washed, then contacted with a
 CC detector agent comprising a detector ON specific for the bcr2-ab12 or
 CC bcr3-ab12 translocation regions and a label. The amount of labelled
 CC detector ON bound to the solid phase is then correlated with the presence
 CC or quantity of CML cells in the patient. The method is to detect or
 CC monitor CML cells in patients. It can also be used prognostically to
 CC assess cytogenetic remission in patients with CML. The method detects
 CC both the bcr2-ab12 and the bcr3-ab12 translocations associated with CML.
 CC The assay does not detect CML in the absence of the ph chromosome, nor
 CC does it detect acute lymphotrophic leukaemia (ALL) even if the ALL
 CC patient has the ph chromosome.
 XX
 SQ Sequence 47 BP; 16 A; 9 C; 10 G; 12 T; 0 other;
 XX
 Query Match 79.2%; Score 19; DB 18; Length 47;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 1 GACCAACTGCTGTGAA 19
 YY 29 GACCAACTGCTGTGAA 47
 DB
 XX
 RESULT 12
 AAT91749
 ID AAT91749 standard; DNA; 47 BP.
 XX
 AC AAT91749;
 XX
 DT 08-JAN-1998 (first entry)
 XX
 DE Primer BB332 for bcr2-ab12 and bcr3-ab12 translocation regions.
 XX
 KW PCR; primer; amplify; polymerase chain reaction; haematopoietic cell;
 KW chronic myelogenous leukaemia; human; bcr2-ab12; translocation region;
 KW cytogenetic remission; ph chromosome; bcr3-ab12; CML cell;
 KW acute lymphotrophic leukaemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO9708339-A1.
 XX
 PD 06-MAR-1997.

PR 28-AUG-1995; 95MO-US10919.
 XX
 ER 25-AUG-1995; 95US-0296258.
 XX
 PA (DADE-) DADE INT INC.
 XX
 PI Brown J, Lockhart-bruce C;
 XX WPI: 1997-179294/16.
 DR
 XX
 PR Detection of chronic myelogenous leukaemia cells - by amplification
 PT of RNA from haematopoietic cells with primers for the bcr2-abl2 and
 PT bcr3-abl2 trans-location regions
 XX
 PS Claim 3; Page 11; 79pp; English.
 CC
 CC AAT91749-T91763, and AAT91765-T91792 are primers used in the method of
 CC the invention AAT91754-T91759 can also be used as capture
 CC oligonucleotides (ON), while AAT91760-T91763, AAT91791 and AAT91792 can
 CC also be used as detector agents. The method of the invention is for
 CC detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
 CC human patient. The method comprises obtaining RNA from haematopoietic
 CC cells of the patient, and amplifying it using a pair of primers that
 CC amplify both the bcr2-abl2 and bcr3-abl2 translocation regions. The
 CC amplified sequence is contacted with a capture agent comprising a capture
 CC ON and a binding ligand to form a capture mixture. The capture ON is
 CC specific for the bcr2-abl2 and bcr3-abl2 translocation regions. The
 CC mixture is contacted with a solid phase coupled to a receptor specific
 CC for the binding ligand. The solid phase is washed, then contacted with a
 CC detector agent comprising a detector ON specific for the bcr2-abl2 or
 CC bcr3-abl2 translocation regions and a label. The amount of labelled
 CC detector ON bound to the solid phase is then correlated with the presence
 CC or quantity of CML cells in the patient. The method is to detect or
 CC monitor CML cells in patients. It can also be used prognostically to
 CC assess cytogenetic remission in patients with CML. The method detects
 CC both the bcr2-abl2 and the bcr3-abl2 translocations associated with CML.
 CC The assay does not detect CML in the absence of the Ph chromosome, nor
 CC does it detect acute lymphoblastic leukaemia (ALL) even if the ALL
 CC patient has the Ph chromosome.
 CC
 SQ Sequence 47 BP; 15 A; 9 C; 10 G; 13 T; 0 other;
 QY 1 GACCAACTCGTGTGTA 17
 Db 31 GACCAACTCGTGTGTA 47
 Query Match 70.8%; Score 17; DB 18; Length 47;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS
 XX
 DE Human leukemia chimera gene Major bcr/abl forward PCR primer.
 XX
 KW Human: PCR: primer; ss: leukaemia; Major-bcr/abl; minor-bcr/abl;
 KM PML/RARalpha; AML1/MTG8; Micro-bcr/abl; TEL/MLL; E2A/PBX1; MLL/AF4;
 KN CBFBeta/Myb1; MLL/AF9; WTI; GAPDH.
 OS
 XX Homo sapiens.
 XX
 PN JP002136300-A.
 XX
 PD 14-MAY-2002.
 XX
 PF 12-DEC-2000; 2000JP-0377325.
 XX

PR 25-AUG-2000; 2000JP-0255570.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 DR WPI: 2002-532069/57.
 XX
 PT A method for detection of leukemia chimera genes of Major-bcr/abl,
 PT minor-bcr/abl, PML/RARalpha and AML1/MTG8 with their specific primer
 PT sets and probes for the diagnosis
 XX
 PS Example 1; Page 9; 20pp; Japanese.
 CC
 CC The invention relates to a novel screening and diagnostic system for
 CC detection of leukemia chimera genes. Included in the disclosure is a
 CC polymerase chain reaction (PCR) method for real time detection of
 CC leukemia chimera genes of Major-bcr/abl, minor-bcr/abl, PML/RARalpha and
 CC AML1/MTG8 with their specific primer sets and probes so as to
 CC simultaneously give PCR amplified product including regions capable of
 CC detection of the genes. The sequences shown in ABQ92608-ABQ92652
 CC represent the primer sets and probes used in the invention.
 CC
 SQ Sequence 22 BP; 4 A; 5 C; 7 G; 6 T; 0 other;
 QY 1 GACCAACTCGTGTGTA 16
 Db 7 GACCAACTCGTGTGTA 22
 Query Match 66.7%; Score 16; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 26+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS
 XX
 DE Forward primer for BCR/ABL type chimera mRNA.
 XX
 KW PCR primer: BCR/ABL type chimera; chimera detection; Major-bcr;
 KW nucleic acid strand based amplification; NASBA method; ss.
 XX
 OS Synthetic.
 XX
 PN JP10229899-A.
 XX
 PD 02-SEP-1998.
 XX
 PE 21-FEB-1997; 97JP-0054092.
 XX
 PR 21-FEB-1997; 97JP-0054092.
 XX
 PA (SRLS-) SRL KK.
 PA (TOYO) TOYOBO KK.
 XX
 DR WPI: 1998-524294/45.
 XX
 PT Forward side primer and reverse side primer - used for detection of
 PT BCR/ABL type chimera mRNA easily with high sensitivity
 XX
 PS Claim 1; Page 6; 8pp; Japanese.
 CC
 CC This sequence represents a primer of the invention used for the detection
 CC of a BCR/ABL type chimera mRNA with a cleavage point in Major-bcr by a
 CC nucleic acid strand based amplification (NASBA) method. The primers can
 CC be used to detect BCR/ABL type chimera mRNA easily with high sensitivity.
 CC
 SQ Sequence 40 BP; 9 A; 13 C; 9 G; 9 T; 0 other;
 QY
 Db
 Query Match 66.7%; Score 16; DB 19; Length 40;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 CGTGTGTAAGTCCA 24
| | | | | | | | | |
DB 1 CGTGTGTAAGTCCA 16

RESULT 15

AAAT03636
ID AAAT03636 standard; DNA; 47 BP.

XX
AC AAAT03636;

DT 02-SEP-1996 (first entry)

DE 3SR primer 325.

XX Self-sustained sequence replication; 3SR; primer; amplification;
KW K562 cell; RNA purification; DNA purification;
KV chronic myelogenous leukaemia; ss.

XX Synthetic.

OS
PN WO9600228-A1.

XX
PD 04-JAN-1996.

XX
PF 23-JUN-1995; 95WO-US07940.

XX
PR 23-JUN-1994; 94US-0264556.

XX
PA (DADE-) DADE INT INC.

XX
PI Brown JT;

XX
DR WPI; 1996-068821/07.

XX
PT Isolating intact nucleic acid from biological samples - using a
PT lysing buffer contg. an ionic detergent, ppty. protein and then
PT ppty. and sepg. nucleic acid

XX
PS Example 3; Page 18; 46pp; English.

XX
CC Primers 325 (AAAT03636) and 329 (AAAT03637) were used for the 3SR
CC amplification of RNA from K562 cells obtd. from a chronic
CC myelogenous leukaemia (CML) patient. The RNA was obtd. using a
CC novel rapid isolation method that involved use of a lysing buffer
CC contg. ionic detergent, ppty. protein, and then ppty. and sepg.
CC the RNA. A probe (AAAT03638) complementary to the junction sequence
CC of the bcr2-abl2 translocation characteristic of CML was used to
CC detect 3SR products, demonstrating that the isolated RNA was a
CC suitable template for 3SR amplification.

XX
SQ Sequence 47 BP; 15 A; 9 C; 10 G; 13 T; 0 other;

Query Match 62.5%; Score 15; DB 17; Length 47;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACCAACTGCTGTGT 15
| | | | | | | | | |
DB 33 GACCAACTGCTGTGT 47

Search completed: December 21, 2002, 11:54:31
Job time : 86.3837 secs

GenCore version 5.1.3
(c) 1993 - 2002 Compu

using sw model

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2002, 02:00:32 ; Search time 85.8163 Seconds
                (without alignments)
                656.052 Million cell updates/sec
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9-6

AGCAATTCGGCTGACC 25

Gapext 1.0

1125999159 residues

ing chosen parameters: 23903332

ch 08

st 45 summaries

011002.*
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cgdat4/genseqd/genseqn-emb1/NA1981.DAT.*
cgdat4/genseqd/genseqn-emb1/NA1982.DAT.*
cgdat4/genseqd/genseqn-emb1/NA1983.DAT.*
cgdat4/genseqd/genseqn-emb1/NA1984.DAT.*
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cgcdat4/genseqd/genseqn-emb1/NA1990.DAT.*
cgcdat4/genseqd/genseqn-emb1/NA1991.DAT.*
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cgcdat4/genseqd/genseqn-emb1/NA2001A.DAT.*
cgcdat4/genseqd/genseqn-emb1/NA2001B.DAT.*
cgcdat4/genseqd/genseqn-emb1/NA2002.DAT.*

er of results predicted by chance to have a equal to the score of the result being printed ysis of the total score distribution.

SUMMARIES

ID	Description
1	AA260848
2	AA260849
3	AA260850
4	AA260851
5	AA260852
6	AA260853
7	AA260854
8	AA260855
9	AA260856
10	AA260857
11	AA260858
12	AA260859
13	AA260860
14	AA260861
15	AA260862
16	AA260863
17	AA260864
18	AA260865
19	AA260866
20	AA260867
21	AA260868
22	AA260869
23	AA260870
24	AA260871
25	AA260872
26	AA260873
27	AA260874
28	AA260875
29	AA260876
30	AA260877
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86	AA260933
87	AA260934
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89	AA260936
90	AA260937
91	AA260938
92	AA260939
93	AA260940
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95	AA260942
96	AA260943
97	AA260944
98	AA260945
99	AA260946
100	AA260947

C	10	18.8	75.2	39	20	AA081653	Probe used to iso
C	11	18	72.0	22	14	AA034655	Human bcr exon 3.5
C	12	18	72.0	62	15	AA066774	L6(1)31 ribozyme s
C	13	18	72.0	81	15	AA066775	L6(1)31 ribozyme.
C	14	17	68.0	20	21	AA029165	PCR primer for bcr
C	15	17	68.0	60	17	AA029713	Chronic myeloid leu
C	16	16	64.0	30	19	AA054411	Chronic myeloid leu
C	17	15.6	62.4	82	22	AA076306	Biotin labelled DN
C	18	15.6	62.4	82	22	AA040843	Human foetal liver
C	19	15.6	62.4	82	22	AA029960	Probe #19309 for g
C	20	15.6	62.4	82	22	AA050952	Human brain expres
C	21	15.6	62.4	82	22	AA127991	Human bone marrow
C	22	15.4	61.6	80	22	AA042656	Probe #17924 for g
C	23	15	60.0	54	13	AA028727	Human spliced tran
C	24	14.8	59.2	65	24	AB028170	Sequence of oligo
C	25	14.6	58.4	65	24	AB051172	Rat spliced trans
C	26	14.6	58.4	90	21	AA028617	Mouse spliced tran
C	27	14.4	57.6	60	24	AB032918	Human secreted pro
C	28	14.4	57.6	60	24	AB033765	Human spliced tran
C	29	14.4	57.6	60	24	AB033903	Human spliced tran
C	30	14.4	57.6	65	24	AB030418	Human spliced tran
C	31	14.2	56.8	28	22	AA049516	Rat spliced trans
C	32	14.2	56.8	35	24	AA087059	Human GRP-binding
C	33	14.2	56.8	39	18	AA078238	PCR primer #2 for
C	34	14.2	56.8	39	18	AA078247	IL-4 2'NH2 RNA li
C	35	14.2	56.8	39	18	AA078229	IL-4 2'NH2 RNA li
C	36	14.2	56.8	47	21	AA026265	Human map-related
C	37	14.2	56.8	60	24	AB045641	Human spliced tran
C	38	14.2	56.8	65	24	AB055069	Human spliced tran
C	39	14.2	56.8	75	24	AB055010	Mouse spliced tra
C	40	14.2	56.8	75	22	AA036839	Mouse spliced tra
C	41	14.2	56.8	75	22	AA036840	Nucleotide sequen
C	42	14	56.0	16	18	AA076900	Human BCR exon I
C	43	14	56.0	20	19	AA056776	Forward primer for
C	44	14	56.0	21	22	AA035411	Human coding seq
C	45	14	56.0	60	24	AB049089	Human spliced tra

ALIGNMENTS

XX	RESULT 1
XX	AAZ60848
XX	AAZ60848 standard; DNA; 25 BP.
XX	AAZ60848;
XX	16-MAY-2000 (first entry)
XX	Oligonucleotide used to detect bcf b3-abl fusion transcripts.
XX	Fusion transcript; translocation; bcr b3 region; abl gene;
XX	amplification assay; detection assay; medical diagnosis; marker;
XX	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX	disease marker; cancer; leukemia; ss.
XX	Synthetic.
XX	WO200005418-A1.
XX	03-FEB-2000.
XX	23-JUL-1999; 99WO-US16832.
XX	23-JUL-1998; 98US-0121239.
XX	(GENP-) GEN-PROBE INC.
XX	Harvey RC, Eastman PS;
XX	WPI; 2000-182730/16.
XX	Novel methods for preparing RNA from biological samples, used for the

PT detection and measurement of nucleic acids and fusion nucleic acids
 XX Claim 19; Page 41; 49pp; English.
 PS
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 25 BP; 5 A; 10 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCACAGCATTCGGTGACC 25
 |||:|||||:|||||:|||||
 Db 1 GACTGTCACAGCATTCGGTGACC 25

RESULT 2
 ID AAZ60849 standard; RNA; 25 BP.
 AC
 XX AAZ60849;

DT 16-MAY-2000 (first entry)

XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

XX Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 XX Claim 19; Page 41; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 25 BP; 5 A; 10 C; 5 G; 5 U; 0 other;

Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 80.0%; Pred. No. 0.032;
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCACAGCATTCGGTGACC 25
 |||:|||||:|||||:|||||
 Db 1 GACUGTCACAGCAUUCGCGUGACC 25

RESULT 3
 ID AAZ60850/c
 AC AAZ60850 standard; DNA; 25 BP.
 XX
 AC AAZ60850;

DT 16-MAY-2000 (first entry)

XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

XX Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 XX Claim 19; Page 41; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

XX Sequence 25 BP; 5 A; 5 C; 10 G; 5 T; 0 other;

SO Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.032; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

OY 1 GACTGTCACAGCATTCGCTGACC 25
 DB 25 GACTGTCACAGCATTCGCTGACC 1

RESULT 4
 AA60851/C
 ID AA60851 standard; RNA; 25 BP.
 XX AA60851;
 AC
 XX
 XX
 DT 16-MAY-2000 (first entry)
 DE
 XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 XX
 XX Fusion transcript; translocation; bcr b3 region; abl gene;
 XX amplification assay; detection assay; medical diagnosis;
 XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 XX disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 XX
 XX WO200005418-A1.
 PN
 XX
 XX 03-FEB-2000.
 PD
 XX
 XX 23-JUL-1999; 99WO-US16832.
 PF
 XX
 XX 23-JUL-1998; 98US-0121239.
 PR
 XX (GENP-) GEN-PROBE INC.
 PA
 XX Harvey RC, Bastman PS;
 PI
 XX WPI; 2000-182730/16.
 DR
 XX
 XX Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids -
 PT
 XX
 XX Claim 19; Page 41; 49pp; English.

PS Oligonucleotides AA60840-62 and AA60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

XX Sequence 25 BP; 5 A; 5 C; 10 G; 5 U; 0 other;

SO Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.032; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

OY 1 GACTGTCACAGCATTCGCTGACC 25
 DB 25 GACTGTCACAGCATTCGCTGACC 1

RESULT 5
 AA046951
 ID AA046951 standard; DNA; 56 BP.
 XX AA046951;
 AC
 XX
 XX
 DT 21-JAN-1994 (first entry)
 DE
 XX Blinded probe to CMLb translocation region of chromosome 22.
 XX
 XX Chronic myelogenous leukaemia; CMLb; abl region;
 XX acute lymphocytic leukaemia; ALL; genetic translocation;
 XX chromosome 22; target sequence; universal detection oligomer;
 XX branched probe; chemiluminescent acridinium ester; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 1..40
 FT misc-feature /tag- a
 FT /note- "complementary to region of chromosome 22
 FT associated with CMLb translocation"
 FT
 FT misc-feature 41..56 /tag- b
 FT /note- "complementary to nucleotides 16-1 of
 FT universal detection probe AA046949"
 FT
 FT
 PN BP552931-A.
 XX
 XX 28-JUL-1993.
 PD
 XX
 XX 20-JAN-1993; 93EP-0300377.
 PF
 XX
 XX 22-JAN-1992; 92US-0827021.
 PR
 XX (GENP-) GEN PROBE INC.
 PA
 XX Arnold LJ, Beverkov R, Hogan JJ, Nelson NC;
 PI
 XX WPI; 1993-236606/30.
 DR
 XX
 XX Nucleic acid molecules which hybridise in presence of target
 PT nucleic acid - are used as probes in hybridisation assays or as
 PT therapeutic agents for diseases
 PT
 XX Example 6; Fig 12B; 56pp; English.

PS Chimeric targets were synthesised homologous to 3 different
 CC genetic translocations between a constant abl region of chromosome
 CC 9 and various regions of chromosome 22; two are the most common
 CC translocations associated with chronic myelogenous leukaemia (CMLa
 CC and CMLb) and the other is associated with acute lymphocytic
 CC leukaemia (ALL). An AE-labelled universal detection oligomer (AA046949)
 CC specific for the abl region was synthesised. Three different
 CC strands were designed to contain a probe region specific for one of
 CC the translocated chromosome 22 regions as well as an arm region

CC complementary to part of the universal probe (AA046950-2). The probe
CC mixes were found to detect only the correct chimeric targets and
CC did not cross-react significantly with the other targets.
XX
SQ Sequence 56 BP; 18 A; 18 C; 9 G; 11 T; 0 other;

Query Match 100.0%; Score 25; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACTGTCCACAGCATTCGCTGAC 25
|||||
DB 3 GACTGTCCACAGCATTCGCTGAC 27

RESULT 6
AA051830
ID AA051830 standard; RNA; 26 BP.
XX
AC AA051830;
XX
DT 26-MAY-1994 (first entry)
XX
DE bcr mRNA ribozyme cleavable nucleotide 3264.

Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
human; chronic myelogenous leukemia; CML; follicular lymphoma;
B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
hairpin; hepatitis delta virus; group I intron; RNaseP; ss.

OS Homo sapiens.
XX
PN W09323057-A.
XX
PD 25-NOV-1993.
XX
PF 13-MAY-1993; 93WO-US04573.
XX
PR 14-MAY-1992; 92US-0882822.
PR 14-MAY-1992; 92US-0882885.
PR 26-AUG-1992; 92US-0936110.
PR 26-AUG-1992; 92US-0936421.
PR 26-AUG-1992; 92US-0936422.
PR 26-AUG-1992; 92US-0936531.
PR 26-AUG-1992; 92US-0936532.
PR 07-DEC-1992; 92US-0987131.
PR 19-JAN-1993; 93US-0006122.
PR 19-JAN-1993; 93US-0008910.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Thompson JD;
XX
WPI; 1993-386203/48.

PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT associated with tumours or mRNA expressed from gene encoding
PT multiple drug resistance
XX
PS Claim 3; Fig 3; 69pp; English.

XX The sequences given in AA051825-2266 represent areas of mRNAs
CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC and lung cancer. The full length mRNAs containing these target
CC sequences, encode aberrant cellular proteins which are able to control
CC cellular proliferation and are directly linked to a leukemic

CC phenotype. These target sequences are identified by the ribozyme of
CC the invention. The ribozymes is formed in a hammerhead motif, but may
CC also be formed in the motif of a hairpin, hepatitis delta virus, group
CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
CC the development or expression of a transformed phenotype in man and
CC other animals by modulating expression of the corresponding gene.
CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC cells elicits inhibition of the transformed state. Multiple drug
CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC drug resistance used by transformed cells and thus enhances drug
CC therapy for tumours. The ribozymes may also be used to study
CC genetic drift and mutations within cells.
SQ Sequence 26 BP; 6 A; 10 C; 5 G; 5 U; 0 other;

Query Match 96.0%; Score 24; DB 14; Length 26;
Best Local Similarity 79.2%; Pred. No. 0.095;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGAC 24
|||||
DB 3 GACTGTCCACAGCATTCGCTGAC 26

RESULT 7
AAV58775
ID AAV58775 standard; DNA; 40 BP.
XX
AC AAV58775;
XX
DT 10-DEC-1998 (first entry)
XX
DE Forward primer for BCR/ABL type chimera mRNA.

PCR primer; BCR/ABL type chimera; chimera detection; Major-bcr;
nucleic acid strand based amplification; NASBA method; ss.

OS Synthetic.
XX
PN JP10229899-A.
XX
PD 02-SEP-1998.
XX
PF 21-FEB-1997; 97JP-0054092.
XX
PR 21-FEB-1997; 97JP-0054092.
XX
PA (SRLS-) SRL KK.
XX
PA (TOYM) TOYOBO KK.
XX
DR WPI; 1998-524294/45.
XX
PT Forward side primer and reverse side primer - used for detection of
PT BCR/ABL type chimera mRNA easily with high sensitivity
XX
PS Claim 1; Page 6; 8pp; Japanese.

XX This sequence represents a primer of the invention used for the detection
CC of a BCR/ABL type chimera mRNA with a cleavage point in Major-bcr by a
CC nucleic acid strand based amplification (NASBA) method. The primers can
CC be used to detect BCR/ABL type chimera mRNA easily with high sensitivity.
XX
SQ Sequence 40 BP; 9 A; 13 C; 9 G; 9 T; 0 other;

Query Match 96.0%; Score 24; DB 19; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGAC 24
|||||
DB 17 GACTGTCCACAGCATTCGCTGAC 40

```

RESULT 8
ID AAT91761/C
AC AAT91761 standard; DNA; 20 BP.
XX
XX AAT91761;
XX
XX 08-JAN-1998 (first entry)
XX
XX Primer DEF350 for bcr2-abl2 and bcr3-abl2 translocation regions.
XX
XX PCR; primer: amplify; polymerase chain reaction; haematopoietic cell;
XX chronic myelogenous leukaemia; human; bcr2-abl2; translocation region;
XX cytogenetic remission; Ph chromosome; bcr3-abl2; CML cell;
XX acute lymphotrophic leukaemia; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 20
XX /*tag= a
XX /note= "amidated"
XX
XX WO9708339-A1.
XX
XX 06-MAR-1997.
XX
XX 28-AUG-1995; 95WO-US10919.
XX
XX 25-AUG-1995; 95US-0296258.
XX
XX (DADE-) DADE INT INC.
XX
XX Brown J, Lockhart-bruce C;
XX
XX WPI; 1997-179294/16.
XX
XX Detection of chronic myelogenous leukaemia cells - by amplification
XX of RNA from haematopoietic cells with primers for the bcr2-abl2 and
XX bcr3-abl2 trans-location regions
XX
XX Claim 11; Page 12; 79pp; English.
XX
XX AAT91749-T91763, and AAT91765-T91792 are primers used in the method of
XX the invention. AAT91754-T91759 can also be used as capture
XX oligonucleotides (ON), while AAT91760-T91763, AAT91791 and AAT91792 can
XX also be used as detector agents. The method of the invention is for
XX detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
XX human patient. The method comprises obtaining RNA from haematopoietic
XX cells of the patient, and amplifying it using a pair of primers that
XX amplify both the bcr2-abl2 and bcr3-abl2 translocation regions. The
XX amplified sequence is contacted with a capture agent comprising a capture
XX ON and a binding ligand to form a capture mixture. The capture ON is
XX specific for the bcr2-abl2 and bcr3-abl2 translocation regions. The
XX mixture is contacted with a solid phase coupled to a receptor specific
XX for the binding ligand. The solid phase is washed, then contacted with a
XX detector agent comprising a detector ON specific for the bcr2-abl2 or
XX bcr3-abl2 translocation regions and a label. The amount of labelled
XX detector ON bound to the solid phase is then correlated with the presence
XX or quantity of CML cells in the patient. The method is to detect or
XX monitor CML cells in patients. It can also be used prognostically to
XX assess cytogenetic remission in patients with CML. The method detects
XX both the bcr2-abl2 and the bcr3-abl2 translocations associated with CML.
XX The assay does not detect CML in the absence of the Ph chromosome, nor
XX does it detect acute lymphotrophic leukaemia (ALL) even if the ALL
XX patient has the Ph chromosome.
XX
XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 other;
XX
XX Query Match 80.0%; Score 20; DB 18; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 6.6;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 TCCACAGCATTCGCTGACC 25

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Db 20 TCCACAGCATTCGCTGACC 1
XXXXXXXXXXXXXXXXXXXX
RESULT 9
ID AAT91782
AC AAT91782 standard; DNA; 45 BP.
XX
XX AAT91782;
XX
XX 08-JAN-1998 (first entry)
XX
XX Primer BB316 for bcr2-abl2 and bcr3-abl2 translocation regions.
XX
XX PCR; primer: amplify; polymerase chain reaction; haematopoietic cell;
XX chronic myelogenous leukaemia; human; bcr2-abl2; translocation region;
XX cytogenetic remission; Ph chromosome; bcr3-abl2; CML cell;
XX acute lymphotrophic leukaemia; ss.
XX
XX Synthetic.
XX
XX WO9708339-A1.
XX
XX 06-MAR-1997.
XX
XX 28-AUG-1995; 95WO-US10919.
XX
XX 25-AUG-1995; 95US-0296258.
XX
XX (DADE-) DADE INT INC.
XX
XX Brown J, Lockhart-bruce C;
XX
XX WPI; 1997-179294/16.
XX
XX Detection of chronic myelogenous leukaemia cells - by amplification
XX of RNA from haematopoietic cells with primers for the bcr2-abl2 and
XX bcr3-abl2 trans-location regions
XX
XX Example 1; Page 11; 79pp; English.
XX
XX AAT91749-T91763, and AAT91765-T91792 are primers used in the method of
XX the invention. AAT91754-T91759 can also be used as capture
XX oligonucleotides (ON), while AAT91760-T91763, AAT91791 and AAT91792 can
XX also be used as detector agents. The method of the invention is for
XX detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
XX human patient. The method comprises obtaining RNA from haematopoietic
XX cells of the patient, and amplifying it using a pair of primers that
XX amplify both the bcr2-abl2 and bcr3-abl2 translocation regions. The
XX amplified sequence is contacted with a capture agent comprising a capture
XX ON and a binding ligand to form a capture mixture. The capture ON is
XX specific for the bcr2-abl2 and bcr3-abl2 translocation regions. The
XX mixture is contacted with a solid phase coupled to a receptor specific
XX for the binding ligand. The solid phase is washed, then contacted with a
XX detector agent comprising a detector ON specific for the bcr2-abl2 or
XX bcr3-abl2 translocation regions and a label. The amount of labelled
XX detector ON bound to the solid phase is then correlated with the presence
XX or quantity of CML cells in the patient. The method is to detect or
XX monitor CML cells in patients. It can also be used prognostically to
XX assess cytogenetic remission in patients with CML. The method detects
XX both the bcr2-abl2 and the bcr3-abl2 translocations associated with CML.
XX The assay does not detect CML in the absence of the Ph chromosome, nor
XX does it detect acute lymphotrophic leukaemia (ALL) even if the ALL
XX patient has the Ph chromosome.
XX
XX Sequence 45 BP; 15 A; 11 C; 8 G; 11 T; 0 other;
XX
XX Query Match 76.0%; Score 19; DB 18; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GACTGTCCACAGCATTCG 19
XXXXXXXXXXXXXXXXXXXX

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DB      27  GACTGTCACAGCATTCGG  45

RESULT 10
AAx81653/c
ID      AAx81653 standard; DNA; 39 BP.
XX
XX
XX      AAx81653;
AC
XX      26-AUG-1999 (first entry)
DT
XX
XX      Probe used to isolate erythrovirus V9 nucleotide sequences.
DE
XX
XX      Erythrovirus V9; differential diagnosis; parvovirus; infection;
KW      erythrovirus screening; typing; immunoassay; probe; ss.
XX
XX      Synthetic.
OS      Erythrovirus.
XX
XX      FR2771751-A1.
PN
XX
XX      04-JUN-1999.
PD
XX
XX      03-DEC-1997; 97FR-0015197.
PF
XX
XX      03-DEC-1997; 97FR-0015197.
PR
XX
XX      (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA
XX
XX      Auguste V, Garbarg CA, Nguyen QT;
PI
XX
XX      WPI: 1999-349543/30.
DR
XX
XX      Erythrovirus V9 and its nucleic acid sequences - can be used in the
PT      diagnosis of its infections
PM
XX
XX      Claim 3; Page 38; 80pp; French.
PS
XX
XX
CC      AAx81630-81666 represent probes used to isolate erythrovirus V9
CC      polynucleotide sequences. Probes and primers derived from erythrovirus
CC      V9 polynucleotide sequences (AAx81580) can be used for differential
CC      diagnosis of erythrovirus (parvovirus) infections by a combination
CC      of amplification and hybridisation assay. The probes can also be
CC      used to assess susceptibility to erythrovirus infection and for
CC      erythrovirus screening and typing. The antibodies can be used in
CC      immunoassays for diagnosis of erythrovirus V9 infections.
CC
XX
XX      Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 other;
SQ
XX
XX
XX      Query Match      75.2%; Score 18.8; DB 20; Length 39;
XX      Best Local Similarity 90.9%; Pred. No. 26;
XX      Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      2 ACTGTCACAGCATTCGGCTGA 23
OY      ||||||||||||||||
XX      33 ACTGTCACAGCATTCGGCGGA 12
DB

RESULT 11
AAQ34635
ID      AAQ34635 standard; CDNA; 22 BP.
XX
XX      AAQ34635;
AC
XX
XX      10-MAY-1993 (first entry)
DT
XX
XX      Human bcr exon 3 5' PCR primer.
DE
XX
XX      Leukaemia; treatment; blast crisis; specific; CML; translocation;
KW      Philadelphia chromosome; chronic myeloid; chronic myelogenous;
XX      leukemia; polymerase chain reaction; ss.
XX
XX      Synthetic.
OS

```

[illegible]

```

XX  . MO9413793-A.
XX  23-JUN-1994.
XX  16-NOV-1993; 93WO-US11144.
XX  04-DEC-1992; 92US-0989852.
XX  (APOL-) APOLLON INC.
XX  Coney LR, Oakes FT, Pachuk CJ;
XX  WPI; 1994-217873/26.
XX  Ribozymes comprising catalytic sequence, two legs and anchor
XX  sequence(s) complementary to substrate mRNA - is used for treatment
XX  of chronic myelogenous leukaemia and acute lymphoblastic leukaemia
XX  Example 1; Page 31; 67pp; English.
XX  This sequence represents a portion of the fusion mRNA L6 which is
XX  expressed by some of the hematopoietic cells of some chronic
XX  myelogenous leukaemia (CML) and acute lymphocytic leukaemia (ALL)
XX  patients. In the L-6 mRNA, abl exon 2 is linked to bcr exon 2, this
XX  is caused by a translocation between chromosomes 9 and 22. The L6
XX  mRNA encodes a protein with aberrant tyrosine kinase activity which is
XX  unique to CML cells and which is thought to play a key role in the
XX  establishment of CML. The ribozymes of the invention are specifically
XX  targeted to the L6, and related K28, mRNAs. Non-contiguous regions of
XX  the substrate RNA can be utilised for the separate events of ribozyme
XX  cleavage and ribozyme cleavage. The ribozymes are targeted to the L6
XX  bcr-abl RNA via an anchor sequence which is proximal to the bcr-abl
XX  junction. Cleavage by these ribozymes occurs at a downstream site
XX  located within an abl specific sequence in the fusion mRNA. Normal abl
XX  and bcr substrates are not cleaved. Ribozymes such as these are useful
XX  in treating diseases involving translocations eg. CML, ALL and
XX  follicular lymphomas. See also AA06774-96.
XX  Sequence 62 BP; 18 A; 19 C; 13 G; 12 U; 0 other:
XX  Query Match 72.0%; Score 18; DB 15; Length 62;
XX  Best Local Similarity 83.3%; Pred. No. 65;
XX  Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 8 CACAGCATTCGCGTGACC 25
   |||||:|||||
Db 1 CACAGCAUUCGCGTGACC 18

RESULT 13
AA06775/c
ID AA06775 standard; RNA; 81 BP.
XX
XX AA06775;
XX 10-FEB-1995 (first entry)
XX
XX L6(1)31 ribozyme.
XX
XX Fusion mRNA; L6; hematopoietic cells; chronic myelogenous leukaemia;
XX CML; acute lymphocytic leukaemia; ALL; exon 2; abl; bcr; exon 3; K28;
XX translocation; chromosome 9; chromosome 22; tyrosine kinase; cleavage;
XX ribozymes; nucleation; anchor sequence; follicular lymphomas; ss.
XX
XX Homo sapiens.
XX
XX Key 1.37 Location/Qualifiers
XX misc_RNA /tag= a
XX /note= "Complementary to abl exon 2"
XX 10..31
XX /tag= b
XX

```

```

XX  . MO9413793-A.
XX  23-JUN-1994.
XX  16-NOV-1993; 93WO-US11144.
XX  04-DEC-1992; 92US-0989852.
XX  (APOL-) APOLLON INC.
XX  Coney LR, Oakes FT, Pachuk CJ;
XX  WPI; 1994-217873/26.
XX  Ribozymes comprising catalytic sequence, two legs and anchor
XX  sequence(s) complementary to substrate mRNA - is used for treatment
XX  of chronic myelogenous leukaemia and acute lymphoblastic leukaemia
XX  Claim 17; Fig 2; 67pp; English.
XX  This sequence represents a ribozyme which binds to and cleaves,
XX  a portion of the fusion mRNA L6 which is expressed by some of the
XX  hematopoietic cells of some chronic myelogenous leukaemia (CML) and
XX  acute lymphocytic leukaemia (ALL) patients. In the L-6 mRNA, abl
XX  exon 2 is linked to bcr exon 2, this is caused by a translocation
XX  between chromosomes 9 and 22. The L6 mRNA encodes a protein with
XX  aberrant tyrosine kinase activity which is unique to CML cells and
XX  which is thought to play a key role in the establishment of CML.
XX  Ribozymes such as these are specifically targeted to the L6, and
XX  related K28, mRNAs. Non-contiguous regions of the substrate RNA can
XX  be utilised for the separate events of ribozyme nucleation and
XX  ribozyme cleavage. The ribozymes are targeted to the L6 bcr-abl
XX  RNA via an anchor sequence which is proximal to the bcr-abl
XX  junction. Cleavage by these ribozymes occurs at a downstream site
XX  located within an abl specific sequence in the fusion mRNA. Normal abl
XX  and bcr substrates are not cleaved. Ribozymes such as these are useful
XX  in treating diseases involving translocations eg. CML, ALL and
XX  follicular lymphomas. See also AA06774-96.
XX  Sequence 81 BP; 23 A; 17 C; 23 G; 18 U; 0 other:
XX  Query Match 72.0%; Score 18; DB 15; Length 81;
XX  Best Local Similarity 100.0%; Pred. No. 67;
XX  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CACAGCATTCGCGTGACC 25
   |||||:|||||
Db 81 CACAGCATTCGCGTGACC 64

RESULT 14
AA291685
ID AA291685 standard; DNA; 20 BP.
XX
XX AA291685;
XX 19-MAY-2000 (first entry)
XX
XX PCR primer for bcr-abl sequence.
XX
XX PCR primer: bcr-abl gene; chromosomal aberration; BCR gene; ABL gene;
XX breakpoint cluster region; aberration detection; ALL, CML, diagnosis;
XX acute lymphocytic leukaemia; chronic myelogenous leukaemia; ss.
XX

```

OS Homo sapiens.
 XX
 PN US6025126-A.
 XX
 PD 15-FEB-2000.
 XX
 PF 28-OCT-1991; 91US-0784222.
 XX
 PR 28-OCT-1991; 91US-0784222.
 XX
 PA (ARCH-) ARCH DEV CORP.
 XX
 PI Westbrook CA;
 XX
 DR WPI; 2000-181800/16.
 XX
 PT Composition comprising two labeled probes hybridizing to different ends
 of a chromosome, useful for diagnosis of acute lymphocytic leukaemia
 (ALL) and/or chronic myelogenous leukaemia (CML) -
 XX
 PS Example 3; Column 19; 18pp; English.
 XX
 CC This sequence represents a PCR primer for the bcr-abl sequence. The
 CC invention relates to a composition comprising at least 2 labeled probes
 CC for detecting a chromosomal aberration involving the BCR (breakpoint
 CC cluster region) and ABL genes, where one probe hybridises to the ABL side
 CC of the chromosomal aberration and the other to the BCR side of the
 CC chromosomal aberration. The probes are long enough to be specifically
 CC detected in cytogenetic analysis. The composition is useful for
 CC diagnosing acute lymphocytic leukaemia (ALL) and/or chronic myelogenous
 CC leukaemia (CML).
 XX
 SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
 Query Match 68.0%; Score 17; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 ACAGCATTCGCTGACC 25
 DB 1 ACAGCATTCGCTGACC 17

RESULT 15
 AAT29713
 ID AAT29713 standard; mRNA; 60 BP.
 XX
 AC AAT29713;
 XX
 DT 17-DEC-1996 (first entry)
 XX
 DE Chronic myeloid leukaemia b2a2-type bcr-abl junction mRNA.
 XX
 KW Chronic myeloid leukaemia; Philadelphia chromosome; bcr-abl junction;
 KW chromosomal translocation; CD34 antigen; b2a2 type junction; I6;
 KW inhibition; ex vivo treatment; therapy; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_recomb 30..31
 FT /tag= a
 FT /label= junction
 FT note= "site where exon 2 of bcr gene is joined to
 exon 2 of abl gene"

XX
 PN W09612803-A1.
 XX
 PD 02-MAY-1996.
 XX
 PF 23-OCT-1995; 95WO-FR01398.
 XX
 PR 24-OCT-1994; 94FR-0012673.

XX
 PA (GENQ) GENSEF.
 XX
 PI Blumenfeld M;
 XX
 DR WPI; 1996-230604/23.
 XX
 PT Ex vivo treatment of chronic myeloid leukaemia - by treating
 isolated CD34 cells with anti-sense oligo:nucleotide specific for
 the bcr-abl junction
 XX
 PS Disclosure; Fig 1; 40pp; French.
 XX
 CC In a novel ex vivo treatment for chronic myeloid leukaemia (CML),
 CC cells which express the CD34 antigen are selected from amongst the
 CC mononuclear cells of a patient in the chronic phase of CML; the CD34+
 CC cells are then treated with an antisense oligonucleotide which is
 CC complementary to the bcr-abl junction and which prevents expression
 CC of the junction region. The present sequence is that of mRNA from
 CC the region around the b2a2-type bcr-abl junction, one of the two
 CC aberrant junctions found in CML sufferers.
 XX
 SQ Sequence 60 BP; 18 A; 18 C; 13 G; 11 U; 0 other;
 Query Match 68.0%; Score 17; DB 17; Length 60;
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 9 ACAGCATTCGCTGACC 25
 DB 1 ACAGCAUUCGCGUGACC 17

Search completed: December 21, 2002, 11:54:34
 Job time : 88.8163 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 : Search time 68.6531 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-13

Perfect score: 20

Sequence: 1 CAAAGGACGAGGAAACAGG 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	21	AAZ60852
2	20	100.0	20	21	AAZ60853
3	20	100.0	20	21	AAZ60854
4	17.4	87.0	78	21	AAZ607229
5	17.4	87.0	96	17	AAZ15289
6	17.4	87.0	96	21	AAZ607233
7	17.4	87.0	96	24	AAZ15255
8	15.8	79.0	51	21	AAZ6522
9	15.8	79.0	51	21	AAZ6523

10	15.2	76.0	41	19	AAZ51110	Maize polymorphic
11	14.8	74.0	41	19	AAZ47858	Maize polymorphic
12	14.8	74.0	66	21	AAZ07230	Rat CRF coding se
13	14.8	74.0	69	21	AAZ07231	Mouse CRF coding
14	14.8	74.0	84	17	AAZ15289	CDNA encoding rat
15	14.8	74.0	84	21	AAZ07232	Rat CRF coding se
16	14.8	74.0	84	21	AAZ15254	Rat CRF coding se
17	14.8	74.0	87	17	AAZ15290	CDNA encoding mous
18	14.8	74.0	87	21	AAZ07234	Mouse CRF coding
19	14.8	74.0	87	21	AAZ172556	Mouse CRF coding
20	14.4	72.0	65	24	ABN55380	Mouse spliced tran
21	14.2	71.0	21	20	AAZ09101	Tumour necrosis fa
22	14.2	71.0	22	24	ABZ92817	G protein-coupled
23	14.2	71.0	35	20	AAZ19366	PCR primer F 51395
24	14.2	71.0	45	16	AAZ08281	Primer for amplify
25	14.2	71.0	60	24	ABN8790	Human spliced tran
26	14.2	71.0	60	24	ABN43121	Human spliced tran
27	14.2	71.0	60	24	ABN6701	Human spliced tran
28	14.2	71.0	65	24	ABN51948	Mouse spliced tran
29	14.2	71.0	66	22	AAZ04774	Synthetic gene shi
30	14.2	71.0	91	22	ABZ49244	Human breast cell
31	14.2	71.0	91	22	ABZ47161	Human foetal liver
32	14.2	71.0	91	22	ABA34253	Probe #12719 for g
33	14.2	71.0	91	22	AAZ15602	Human brain expres
34	14.2	71.0	91	22	AAZ1335	Human bone marrow
35	14.2	71.0	91	22	AAZ1337	Probe #15063 used
36	14.2	71.0	91	22	AAZ10777	Probe #7768 used t
37	14.2	71.0	91	22	ABZ15342	Human genome-deriv
38	14.2	70.0	60	24	ABN45162	Human spliced tran
39	13.8	69.0	51	19	AAZ5919	Regenaria agrestis
40	13.8	69.0	51	22	AAZ38376	Human SNP flanking
41	13.8	69.0	60	24	ABN40567	Human spliced trans
42	13.8	69.0	65	24	ABN28815	Rat spliced trans
43	13.8	69.0	66	14	AAZ050174	Virus vector fusio
44	13.8	69.0	66	15	AAZ057956	Plant integument p
45	13.8	69.0	75	14	AAZ050175	Virus vector fusio

ALIGNMENTS

RESULT 1	
AAZ60852	16-MAY-2000 (first entry)
ID	AAZ60852 standard; DNA: 20 BP.
XX	AAZ60852;
AC	
XX	
XX	16-MAY-2000 (first entry)
DT	
XX	Oligonucleotide used to detect bcr b3-abl fusion transcripts.
DE	
XX	Fusion transcript; translocation; bcr b3 region; abl gene;
KW	amplification assay; detection assay; medical diagnosis;
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW	disease marker; cancer; leukemia; ss.
XX	
OS	Synthetic.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
PF	23-JUL-1999; 99WO-US16832.
XX	
PR	23-JUL-1998; 98US-0121239.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Harvey RC, Eastman PS;
XX	
DR	WPI: 2000-182730/16.
XX	
PT	Novel methods for preparing RNA from biological samples, used for the

PT detection and measurement of nucleic acids and fusion nucleic acids -
XX
XX Claim 19; Page 42; 49pp; English.
XX
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.
XX

SQ Sequence 20 BP; 9 A; 2 C; 9 G; 0 U; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAAGGACGAGGAGAAGG 20
DB 1 CAAAGGACGAGGAGAAGG 20
|||||

RESULT 2

AAZ60853/c
ID AAZ60853 standard; DNA; 20 BP.

XX
AC AAZ60853;

XX
DT 16-MAY-2000 (first entry)

XX
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX
KW Fusion transcript; translocation; bcr b3 region; abl gene;

XX
KW amplification assay; detection assay; medical diagnosis;

XX
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX
KW disease marker; cancer; leukemia; ss.

XX
OS Synthetic.

XX
PN WO200005418-A1.

XX
PD 03-FEB-2000.

XX
PF 23-JUL-1999; 99WO-US16832

XX
PR 23-JUL-1998; 98US-0121239.

XX
PA (GENP-) GEN-PROBE INC.

XX
PI Harvey RC, Eastman PS;

XX
DR WPI; 2000-182730/16.

XX
PT Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids -

XX
PS Claim 19; Page 42; 49pp; English.

CC
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.
XX

SQ Sequence 20 BP; 0 A; 9 C; 2 G; 9 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAAGGACGAGGAGAAGG 20
DB 20 CAAAGGACGAGGAGAAGG 1
|||||

RESULT 3

AAZ60854/c
ID AAZ60854 standard; RNA; 20 BP.

XX
AC AAZ60854;

XX
DT 16-MAY-2000 (first entry)

XX
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX
KW Fusion transcript; translocation; bcr b3 region; abl gene;

XX
KW amplification assay; detection assay; medical diagnosis;

XX
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX
KW disease marker; cancer; leukemia; ss.

XX
OS Synthetic.

XX
PN WO200005418-A1.

XX
PD 03-FEB-2000.

XX
PF 23-JUL-1999; 99WO-US16832

XX
PR 23-JUL-1998; 98US-0121239.

XX
PA (GENP-) GEN-PROBE INC.

XX
PI Harvey RC, Eastman PS;

XX
DR WPI; 2000-182730/16.

XX
PT Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids -

XX
PS Claim 19; Page 42; 49pp; English.

CC
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

XX Sequence 20 BP; 0 A; 9 C; 2 G; 9 U; 0 other;

SO Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGCAGAGAG 20
 DB 20 CAAGAGCAGCAGCAGAGAG 1

RESULT 4
 ID AAA07229 standard: DNA; 78 BP.
 XX AAA07229;
 XX 22-JUN-2000 (first entry)
 XX Human CRIF coding sequence fragment.
 XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
 XX anxiety disorder; thyrotropin releasing hormone; TRH sequence; human;
 XX general anxiety disorder; panic disorder; obsessive compulsive disorder;
 XX post-traumatic stress disorder; therapy; ss.
 XX Homo sapiens.
 XX US6039956-A.
 XX 21-MAR-2000.
 XX 07-JUN-1996; 96US-0660561.
 XX 12-SEP-1994; 94US-0304383.
 XX 08-SEP-1995; 95US-0523125.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX McGivenn RF, Rittenhouse PA, Aird F, Redel E;
 XX WPI: 2000-270120/23.
 XX P-PSDB: AAY81900.
 XX Treating behavioural symptoms including panic disorder, post-traumatic
 XX stress disorder and obsessive compulsive disorder in humans, involves
 XX administering corticotropin release inhibiting factor -
 XX Disclosure; Column 2; 43pp; English.

XX This sequence encodes a human corticotropin release inhibitory factor
 CC (CRIF) fragment. The invention relates to a method for treating (I)
 CC behavioural symptoms in an anxiety disorder in a human, comprising
 CC administering CRIF which comprises 3 contiguous amino acids contained
 CC within the amino acid sequence positioned between the fourth and fifth
 CC thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (I)
 CC is useful for treating behavioural symptoms in an anxiety disorder which
 CC includes general anxiety disorder, panic disorder, obsessive compulsive
 CC disorder and post-traumatic stress disorder. Peripheral administration of
 CC CRIF is capable of crossing the blood-brain barrier.

SO Sequence 78 BP; 28 A; 12 C; 31 G; 7 T; 0 other;

XX Query Match 87.0%; Score 17.4; DB 21; Length 78;
 XX Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGCAGAGAG 19
 DB 19 CAAGAGCAGCAGCAGAGAG 37

RESULT 5
 ID AAT15289 standard: cDNA; 96 BP.
 XX AAT15289;
 XX 28-OCT-1996 (first entry)
 XX cDNA encoding human prepro-TRH peptide having CRIF activity.
 XX TRH; thyrotropin release factor; Cushing's disease; anxiety;
 XX corticotropin release inhibiting factor; CRIF; depression; obesity;
 XX anorexia nervosa; withdrawal; hypocortisolism; colitis; autoimmune;
 XX arthritis; premenstrual syndrome; inflammatory; obsessive compulsive;
 XX disorder; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX FT 1..96
 XX CDS /*tag= a
 XX /note= "no start or stop codon"
 XX WO9608265-A1.
 XX 21-MAR-1996.
 XX 08-SEP-1995; 95WO-US11455.
 XX 12-SEP-1994; 94US-0304383.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Aird F, Redel E;
 XX WPI: 1996-179720/18.
 XX P-PSDB: AAR95846.
 XX New isolated corticotropin release inhibiting factor peptide(s)
 XX used to develop prods. for the diagnosis and treatment of CRIF
 XX related disorders, e.g. stress responses or inflammation
 XX Claim 16; Page 40; 66pp; English.

XX AAT15289 is a human cDNA sequence encoding a portion of the prepro-TRH
 CC (thyrotropin releasing hormone) protein positioned between the
 CC fourth and fifth TRH sequences (amino acids 158-183). The peptide
 CC encoded has CRIF (corticotropin release inhibiting factor) activity
 CC and may be used for the diagnosis and treatment of CRIF related
 CC disorders. Such disorders include Cushing's disease, anxiety, anorexia
 CC nervosa, depression, obesity, withdrawal from drug or alcoholic
 CC dependency, some cancers, hypocortisolism, ACTH (adrenocorticotropin)
 CC deficiency, premenstrual syndrome, inflammatory conditions e.g.
 CC colitis and autoimmune disease e.g. arthritis. Peptides with CRIF
 CC activity may also be used to enhance immune responses and to increase
 CC the efficacy of immunity to vaccines.

XX Sequence 96 BP; 34 A; 18 C; 37 G; 7 T; 0 other;

SO Query Match 87.0%; Score 17.4; DB 17; Length 96;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGAGAG 19
 |||||
 Db 37 CAAAGGAGCTGGGAGAGAG 55

RESULT 6
 ID AAA07233
 AC AAA07233 standard; DNA; 96 BP.

XX
 AC AAA07233;

DT 22-JUN-2000 (first entry)

XX Human CRIF coding sequence fragment.

XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
 KW anxiety disorder; thyrotropin releasing hormone; TRH sequence; human;
 KW general anxiety disorder; panic disorder; obsessive compulsive disorder;
 KW post-traumatic stress disorder; therapy; ss.

XX Homo sapiens.

XX US6039956-A.

XX 21-MAR-2000.

PF 07-JUN-1996; 96US-0660561.

XX 12-SEP-1994; 94US-0304383.

PR 08-SEP-1995; 95US-0523125.

XX (UNPE-) UNIV PENNSYLVANIA.

PI McGivenn RF, Rittenhouse PA, Aird F, Redel E;

DR WPI: 2000-270120/23.

PT Treating behavioural symptoms including panic disorder, post-traumatic
 stress disorder and obsessive compulsive disorder in humans; involves
 PT administering corticotropin release inhibiting factor -

PS Disclosure; Column 3; 43pp; English.

XX This sequence encodes a human corticotropin release inhibitory factor
 CC (CRIF) fragment. The invention relates to a method for treating (1)
 CC behavioural symptoms in an anxiety disorder in a human, comprising
 CC administering CRIF which comprises 3 contiguous amino acids contained
 CC within the amino acid sequence positioned between the fourth and fifth
 CC thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (1)
 CC is useful for treating behavioural symptoms in an anxiety disorder which
 CC includes general anxiety disorder, panic disorder, obsessive compulsive
 CC disorder and post-traumatic stress disorder. Peripheral administration of
 CC CRIF is capable of crossing the blood-brain barrier.

XX Sequence 96 BP; 34 A; 18 C; 37 G; 7 T; 0 other;

Query Match 87.0%; Score 17.4; DB 21; Length 96;

Best Local Similarity 94.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGAGAG 19
 |||||
 Db 37 CAAAGGAGCTGGGAGAGAG 55

RESULT 7
 ID AAI72555

XX AAI72555 standard; cDNA; 96 BP.

AC AAI72555;

DT 21-MAY-2002 (first entry)

XX Human CRIF coding sequence.

DE Rat; human; mouse; gene; corticotropin release inhibiting factor;
 KW CRIF; ACTH; adrenocorticotropin; TRH; prepro; behavioural disorder;
 KW thyrotropin releasing hormone; Cushing's disease; panic disorder;
 KW obsessive compulsive disorder; anorexia nervosa; depression; anxiety;
 KW obesity; alcohol dependence; drug dependence; premenstrual syndrome;
 KW chronic stress related syndrome; autoimmune disease; cancer;
 KW chronic fatigue syndrome; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT 19..96
 FT CDS /*tag= a
 FT /note= "Encodes prepro human TRH 158-183"

XX US6348571-B1.

XX 19-FEB-2002.

PF 03-AUG-1999; 99US-0366627.

XX 12-SEP-1994; 94US-0304383.

PR 08-SEP-1995; 95US-0523125.

XX 07-JUN-1996; 96US-0660561.

PA (NCUN) UNIV NORTHWESTERN.

XX (UNPE-) UNIV PENNSYLVANIA.

PI Redel E, Aird F;

DR WPI: 2002-237138/29.

DR P-P-SDB; AAB47924.

PT A corticotropin release inhibiting factor peptide, useful for treating
 behavioural disorders in mammals, particularly humans e.g. anxiety
 PT disorders, depression, anorexia and drug withdrawal -

PS Disclosure; Fig 10; 24pp; English.

XX The sequences given in AAI72554-56 encode rat, human and mouse
 CC corticotropin release inhibiting factor (CRIF), respectively. CRIF
 CC peptides regulate ACTH (adrenocorticotropin) production. The CRIF
 CC peptide of the invention consists of 3-21 residues positioned within
 CC the amino acids sequence positioned between the fourth and fifth TRH
 CC sequence on a prepro-TRH protein (preprothyrotropin releasing hormone).
 CC The CRIF peptide is useful for treating behavioural disorders in
 CC mammals, especially humans, including Cushing's disease, anxiety
 CC disorders (e.g. panic disorder, obsessive compulsive disorder),
 CC anorexia nervosa, depression, obesity, withdrawal from alcohol and drug
 CC dependence, chronic stress related syndromes, autoimmune disease,
 CC chronic fatigue syndrome, premenstrual syndrome, and some cancers
 CC (those where an enhanced autoimmune response reduces the severity of
 CC the disease).

XX Sequence 96 BP; 34 A; 18 C; 37 G; 7 T; 0 other;

Query Match 87.0%; Score 17.4; DB 24; Length 96;

Best Local Similarity 94.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGAGAG 19
 |||||
 Db 37 CAAAGGAGCTGGGAGAGAG 55

RESULT 8
 ID AAA76522/c

XX AAA76522 standard; cDNA; 51 BP.

AC AAA76522;

DT	16-NOV-2000	(first entry)	
DE	Human clone cg20723460	polymorphic site, SEQ ID NO:205.	
KW	Human: single nucleotide polymorphism; SNP;		
KW	detection; identification; gene therapy; ss.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	variation	(26,T)	
FT	*tag= a		
PN	W0200029623-A2.		
PD	25-MAY-2000.		
PF	17-NOV-1999;	99MO-U527293.	
PR	17-NOV-1998;	98US-0109024.	
PR	16-NOV-1999;	99US-0109024.	
PA	(CURA-) CURAGEN CORP.		
PI	Shimketa RA, Leach MD;		
XX	WPI; 2000-387826/33.		
XX	Human nucleic acids containing single nucleotide polymorphisms, useful		
XX	for treating a subject suffering, or at risk from a pathology due to		
XX	the presence of a sequence polymorphism -		
XX	Claim 1: Page 220; 543bp; English.		
XX	Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences		
XX	which contain single nucleotide polymorphisms (SNPs). Sequences 1 to		
XX	1112 (AAA76318-A77429) are consecutive pairs of nucleotides which		
XX	constitute silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are		
XX	consecutive pairs of nucleotides containing SNPs which result in changes		
XX	in the corresponding amino acid sequences (AAB11749-B11928). The SNPs in		
XX	sequences 1113 to 1128 (AAA7430-A77445) lead to conservative amino acid		
XX	changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result		
XX	in non-conservative changes. The SNPs in sequences 1187 to 1192		
XX	(AAA77504-A77509) generate frameshift mutations. The invention also		
XX	relates to a method of detecting a polymorphic site in a nucleic acid and		
XX	a method of determining the relatedness of two nucleic acids. It also		
XX	encompasses peptides containing polymorphic sites, antibodies raised		
XX	against such peptides, and a method of detecting polymorphic		
XX	protein/peptides using the antibodies. The nucleic acids are useful for		
XX	gene therapy of an individual having, suspected of having, or at risk of		
XX	developing a pathological condition due to the presence of a sequence		
XX	polymorphism. Such treatment would comprise administration of the		
XX	wild-type nucleic acid sequence. Antibodies raised against polymorphic		
XX	peptides can also be used in the treatment of such individuals.		
XX	Sequence 51 BP; 10 A; 24 C; 2 G; 15 T; 0 other;		
XX	Sequence 51 BP; 10 A; 24 C; 2 G; 15 T; 0 other;		
XX	Quality Match	79.0%; Score 15.8; DB 21;	
XX	Best Local Similarity	89.5%; Pred. No. 8.9e+02;	
XX	Matches 17; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
XX	QY	2 AAAGGACGAGCAAGAG 20	
XX			
XX	DB	47 AAAGGCGCAAGCAAGAG 29	
XX	RESULT 9		
XX	AAA76523/C		
XX	ID	AAA76523 standard; CDNA: 51 BP.	
XX	AC	AAA76523;	

DT	16-NOV-2000	(first entry)
XX	Human clone cg20723460 polymorphic site, SEQ ID NO:206.	
DE		
XX	Human; single nucleotide polymorphism; SNP;	
KM	detection; identification; gene therapy; ss.	
OS	Homo sapiens.	
XX		
XX	Key location/Qualifiers	
FT	variation /replace (26,C)	
ET	/tag= a	
XX		
PN	W0200029623-A2.	
PD		
XX	25-MAY-2000.	
PF		
XX	17-NOV-1999; 99MO-US27293.	
XX		
PR	17-NOV-1998; 98US-0109024.	
PR	16-NOV-1999; 99US-0109024.	
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Shinkets RA, Leach MD;	
DR	WPI; 2000-387826/33.	
XX		
PT	Human nucleic acids containing single nucleotide polymorphisms, useful	
PT	for treating a subject suffering, or at risk from a pathology due to	
PT	the presence of a sequence polymorphism -	
XX		
PS	Claim 1, Page 220; 543pp; English.	
XX		
CC	Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences	
CC	which contain single nucleotide polymorphisms (SNPs). Sequences 1 to	
CC	1112 (AAA76318-A77429) are consecutive pairs of nucleotides which	
CC	contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are	
CC	consecutive pairs of nucleotides containing SNPs which result in changes	
CC	in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in	
CC	sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid	
CC	changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result	
CC	in non-conservative changes. The SNPs in sequences 1187 to 1192	
CC	(AAA77504-A77509) generate frameshift mutations. The invention also	
CC	relates to a method of detecting a polymorphic site in a nucleic acid and	
CC	a method of determining the relatedness of two nucleic acids. It also	
CC	encompasses peptides containing polymorphic sites, antibodies raised	
CC	against such peptides, and a method of detecting polymorphic	
CC	proteins/peptides using the antibodies. The nucleic acids are useful for	
CC	gene therapy of an individual having, suspected of having, or at risk of	
CC	developing a pathological condition due to the presence of a sequence	
CC	polymorphism. Such treatment would comprise administration of the	
CC	wild-type nucleic acid sequence. Antibodies raised against polymorphic	
CC	peptides can also be used in the treatment of such individuals.	
SQ		
Sequence	51 BP; 10 A; 23 C; 2 G; 16 T; 0 other;	
Query Match	79.0%; Score 15.8; DB 21; Length 51;	
Best Local Similarity	89.5%; Pred. No. 8.9e+02;	
Matches 17; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
OY	2 AAAGGACGCGAGAAGG 20	
DB	47 AAAGGGCAAGGAAGG 29	
RESULT 10		
AAVS1110		
ID	AAVS1110 standard; DNA; 41 BP.	
AC	AAVS1110;	
XX		
DT	11-JAN-1999 (first entry)	

```

XX Maize polymorphic marker S28G5/G6-3 DNA.
DE Polymorphic marker; allele-specific; primer; probe; amplification;
PF hybridisation; plant; hybrid certification; genetic contribution;
XX progeny; back-cross; hybrid; ancestry; maize; ss.
XX Zea mays.
OS
XX
XX Key Location/Qualifiers
XX Variation 21
XX /*tag= a
XX /replace= "a"
XX /note= "polymorphism"
XX
XX W09824796-A1.
XX
XX 11-JUN-1998.
XX
XX 01-DEC-1997; 97WO-US21782.
XX
XX 07-MAR-1997; 97US-0813507.
XX
XX 02-DEC-1996; 96US-0032069.
XX
XX (AFRY-) AFFYMETRIX INC.
XX
XX Landry BS, Lemieux B, Murgieux A, Sapolsky RJ;
XX WPI; 1998-333252/29.
XX
XX Brassica species allele-specific oligonucleotide probes and primers
XX - useful for plant breeding
XX
XX Claim 1; Page 46; 65pp; English.
XX
XX This DNA sequence is a region of a Zea mays genome which contains a
XX polymorphic marker. This sequence can be used in the construction of
XX allele-specific primers and probes for amplification or hybridisation,
XX e.g. to determine common or disparate ancestry between 2 or more plants,
XX to monitor the genetic contribution of an ancestral plant, to trace the
XX progeny of proprietary plants, in certification of a hybrid plant or to
XX identify the progeny of a back-crossed plant with an ancestral plant.
XX
XX Sequence 41 BP; 12 A; 7 C; 19 G; 3 T; 0 other;
SQ
Query Match 76.0%; Score 15.2; DB 19; Length 41;
Best Local Similarity 85.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAAAGGACGAGGAGAAGG 20
Db 6 CCATGACGACGAGGAGAAGG 25
RESULT 11
AAV47858
ID AAV47858 standard; DNA: 41 BP.
XX
XX AAV47858;
XX
XX 14-OCV-1998 (first entry)
XX
XX Maize polymorphic site oligonucleotide marker UMC21-G5/G6-3.
DE
XX
XX Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KW polymorphic site; corn; gramineae species; ss.
XX
XX Synthetic.
OS
XX
XX zeo sp.
PN W09830717-A2.
XX
XX 16-JUL-1998.
PD

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XX 02-DEC-1997; 97WO-EP07134.
XX
XX 02-DEC-1996; 96US-0032069.
XX
XX (BIOC-) BIOCEM SA.
XX
XX Murgieux A;
XX WPI; 1998-399160/34.
XX
XX Claim 2; Page 14; 32pp; English.
XX
XX The present invention describes a nucleic acid segment comprising at
XX least 10 contiguous nucleotides from a vegetal sequence including a
XX polymorphic site which is a single nucleotide polymorphism (SNP), or the
XX complement of the segment. Also described are: (1) an allele-specific
XX oligonucleotide hybridising to segment, or their complements, and (2) a
XX method of analysing nucleic acids from a subject, by determining if a
XX base is occupying any one (or a set) of polymorphic sites in 261
XX sequences derived from six maize lines (see AAV47701 to AAV47961). The
XX segments are useful in fingerprint analysis in plants to determine which
XX polymorphisms are present, which strain a plant belongs to and to
XX distinguish between strains. The polymorphisms may correlate with
XX phenotypic traits (e.g. plant growth rate or crop yield), and the
XX segments are useful to determine the presence/absence of specific
XX polymorphisms correlating with the existence/absence of particular
XX traits. The segments are also useful in marker assisted back-cross
XX techniques to select plants with a higher percentage of recurrent parent
XX in a back-cross population. Segments incorporate SNPs which occur more
XX frequently than other polymorphism types and are therefore more likely
XX to be located close to genetic loci of interest; different forms of
XX characterised SNPs are also often easier to detect than other
XX polymorphism types.
XX
XX Sequence 41 BP; 12 A; 7 C; 18 G; 3 T; 1 other;
SQ
Query Match 74.0%; Score 14.8; DB 19; Length 41;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAAAGGACGAGGAGAAGG 20
Db 6 CCATGACGACGAGGAGAAGG 25
RESULT 12
AAA07230
ID AAA07230 standard; DNA: 66 BP.
XX
XX AAA07230;
XX
XX 22-JUN-2000 (first entry)
XX
XX Rat CR1F coding sequence fragment.
DE
XX
XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
KW anxiety disorder; thyrotropin releasing hormone; TRH sequence; rat;
KW general anxiety disorder; panic disorder; obsessive compulsive disorder;
KW post-traumatic stress disorder; therapy; ss.
XX
XX Rattus sp.
OS
XX
XX US6039956-A.
PN
XX
XX 21-MAR-2000.
PD
XX
XX 07-JUN-1996; 96US-0660561.
PF
XX

```

PR 12-SEP-1994; 94US-0304383.
 PR 08-SEP-1995; 95US-0523125.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 PI McGovern RF, Rittenhouse PA, Aird F, Redel E;
 DR WPI: 2000-270120/23.
 DR P-PSDB; AAY81902.
 XX
 XX Treating behavioural symptoms including panic disorder, post-traumatic
 PT stress disorder and obsessive compulsive disorder in humans, involves
 PT administering corticotropin release inhibiting factor
 XX
 PS Disclosure; Column 2; 43pp; English.
 CC This sequence encodes a rat corticotropin release inhibitory factor
 CC (CRIF) fragment. The invention relates to a method for treating (1)
 CC behavioural symptoms in an anxiety disorder in a human, comprising
 CC administering CRIF which comprises 3 contiguous amino acids contained
 CC within the amino acid sequence positioned between the fourth and fifth
 CC thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (1)
 CC is useful for treating behavioural symptoms in an anxiety disorder which
 CC includes general anxiety disorder, panic disorder, obsessive compulsive
 CC disorder and post-traumatic stress disorder. Peripheral administration of
 CC CRIF is capable of crossing the blood-brain barrier.
 SQ Sequence 66 BP; 22 A; 11 C; 21 G; 12 T; 0 other;
 Query Match 74.0%; Score 14.8; DB 21; Length 66;
 Best Local Similarity 88.9%; Pred. No. 2.4e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGGAGCGAGGAGAA 18
 DB 19 CAAGGAGCTGGGAGAA 36
 RESULT 13
 AAA07231 standard; DNM; 69 BP.
 ID AAA07231;
 AC AAA07231;
 XX
 XX 22-JUN-2000 (first entry)
 DT
 XX
 DE Mouse CRIF coding sequence fragment.
 XX
 XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
 KW anxiety disorder; thyrotropin releasing hormone; TRH sequence; mouse;
 KW general anxiety disorder; panic disorder; obsessive compulsive disorder;
 KW post-traumatic stress disorder; therapy; ss.
 XX
 OS Mus sp.
 XX
 XX US6039956-A.
 PN
 XX 21-MAR-2000.
 PD
 XX
 XX 07-JUN-1996; 96US-0660561.
 PE
 XX 12-SEP-1994; 94US-0304383.
 PR 08-SEP-1995; 95US-0523125.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 PI McGovern RF, Rittenhouse PA, Aird F, Redel E;
 DR WPI: 2000-270120/23.
 DR P-PSDB; AAY81903.
 XX
 XX Treating behavioural symptoms including panic disorder, post-traumatic
 PT stress disorder and obsessive compulsive disorder in humans, involves

PT administering corticotropin release inhibiting factor
 XX
 XX Disclosure; Column 2; 43pp; English.
 XX
 XX This sequence encodes a mouse corticotropin release inhibitory factor
 CC (CRIF) fragment. The invention relates to a method for treating (1)
 CC behavioural symptoms in an anxiety disorder in a human, comprising
 CC administering CRIF which comprises 3 contiguous amino acids contained
 CC within the amino acid sequence positioned between the fourth and fifth
 CC thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (1)
 CC is useful for treating behavioural symptoms in an anxiety disorder which
 CC includes general anxiety disorder, panic disorder, obsessive compulsive
 CC disorder and post-traumatic stress disorder. Peripheral administration of
 CC CRIF is capable of crossing the blood-brain barrier.
 SQ Sequence 69 BP; 22 A; 11 C; 24 G; 12 T; 0 other;
 Query Match 74.0%; Score 14.8; DB 21; Length 69;
 Best Local Similarity 88.9%; Pred. No. 2.4e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGGAGCGAGGAGAA 18
 DB 19 CAAGGAGCTGGGAGAA 36
 RESULT 14
 AAT15288 standard; CDNA; 84 BP.
 ID AAT15288;
 AC AAT15288;
 XX
 XX 28-OCT-1996 (first entry)
 DT
 XX
 DE CDNA encoding rat prepro-TRH peptide having CRIF activity.
 XX
 XX TRH; thyrotropin release factor; Cushing's disease; anxiety;
 KW corticotropin release inhibiting factor; CRIF; depression; obesity;
 KW anorexia nervosa; withdrawal; hypocortisolism; colitis; autoimmune;
 KW arthritis; premenstrual syndrome; inflammatory; obsessive compulsive;
 disorder; ss.
 XX
 OS Rattus rattus.
 XX
 XX
 XX Key Location/Qualifiers
 FH 1.84
 FT CDS /*tag= a
 FT /note= "no start or stop codon"
 FT
 XX WC9608265-A1.
 PN
 XX 21-MAR-1996.
 PD
 XX
 XX 08-SEP-1995; 95WO-US11455.
 PE
 XX 12-SEP-1994; 94US-0304383.
 PR
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 PI Aird F, Redel E;
 XX
 XX WPI: 1996-179720/18.
 DR P-PSDB; AAR95845.
 XX
 XX New isolated corticotropin release inhibiting factor peptide(s)
 PT used to develop prods. for the diagnosis and treatment of CRIF
 PT related disorders, e.g. stress responses or inflammation
 XX
 XX Claim 14; Fig 10; 66pp; English.
 PS
 XX AAT15288 is a rat CDNA sequence encoding a portion of the prepro-TRH
 CC (thyrotropin releasing hormone) protein positioned between the
 CC fourth and fifth TRH sequences (amino acids 178-199). The peptide

CC encoded has CRIF (corticotropin release inhibiting factor) activity
 CC and may be used for the diagnosis and treatment of CRIF related
 CC disorders. Such disorders include Cushing's disease, anxiety, anorexia
 CC nervosa, depression, obesity, withdrawal from drug or alcoholic
 CC dependence, some cancers, hypercortisolism, ACHN (adrenocorticotropin)
 CC deficiency, premenstrual syndrome, inflammatory conditions e.g.
 CC colitis and autoimmune disease e.g. arthritis. Peptides with CRIF
 CC activity may also be used to enhance immune responses and to increase
 CC the efficacy of immunity to vaccines.

SQ Sequence 84 BP; 27 A; 17 C; 27 G; 13 T; 0 other;

Query Match 74.0%; Score 14.8; DB 17; Length 84;

Best Local Similarity 88.9%; Pred. No. 2.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAA 18
 ||||| |||||
 DB 37 CAAAGAGCTGGAGAGAA 54

RESULT 15

AAA07232
 ID AAA07232 standard; DNA; 84 BP.

AC AAA07232;

DT 22-JUN-2000 (first entry)

DE Rat CRIF coding sequence fragment.

KW Corticotropin release inhibitory factor; CRIF; behavioural symptom;
 KW anxiety disorder; thyrotropin releasing hormone; TRH sequence; rat;
 KW general anxiety disorder; panic disorder; obsessive compulsive disorder;
 KW post-traumatic stress disorder; therapy; ss.

OS Rattus sp.

PN US6039956-A.

PD 21-MAR-2000.

PF 07-JUN-1996; 96US-0660561.

PR 12-SEP-1994; 94US-0304383.

PR 08-SEP-1995; 95US-0523125.

PA (UYPE-) UNIV PENNSYLVANIA.

PI McGovern RF, Rittenhouse PA, Aird F, Redei E;

DR WPI; 2000-270120/23.

PT Treating behavioural symptoms including panic disorder, post-traumatic
 PT stress disorder and obsessive compulsive disorder in humans, involves
 PT administering corticotropin release inhibiting factor -
 PS Disclosure; Column 3; 43pp; English.

CC This sequence encodes a rat corticotropin release inhibitory factor
 CC (CRIF) fragment. The invention relates to a method for treating (I)
 CC behavioural symptoms in an anxiety disorder in a human, comprising
 CC administering CRIF which comprises 3 contiguous amino acids contained
 CC within the amino acid sequence positioned between the fourth and fifth
 CC thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (I)
 CC is useful for treating behavioural symptoms in an anxiety disorder which
 CC includes general anxiety disorder, panic disorder, obsessive compulsive
 CC disorder and post-traumatic stress disorder. Peripheral administration of
 CC CRIF is capable of crossing the blood-brain barrier.

SQ Sequence 84 BP; 27 A; 17 C; 27 G; 13 T; 0 other;

Query Match 74.0%; Score 14.8; DB 21; Length 84;

Best Local Similarity 88.9%; Pred. No. 2.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAA 18
 ||||| |||||
 DB 37 CAAAGAGCTGGAGAGAA 54

Search completed: December 21, 2002, 11:54:37
 Job time : 71.6531 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 : Search time 92.6816 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-22

Sequence: 1 JCTGACTTGAGCCTCAGGCTGAGT 27

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: N_Geneseq_101002.*
- 2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
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- 4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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- 21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
- 24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	27	100.0	27	AAZ60859
2	27	100.0	27	AAZ60860
3	27	100.0	27	AAZ60861
4	27	100.0	27	AAZ60862
5	27	100.0	27	AAZ60840
6	27	100.0	27	AAZ60841
7	27	100.0	27	AAZ60842
8	27	100.0	27	AAZ60843
9	26	96.3	80	AAQ34631

10	26	96.3	80	AAV20460
11	24	88.9	50	AAQ86626
12	24	88.9	50	AAI42417
13	24	88.9	50	AAI15571
14	24	88.9	50	AAI66349
15	24	88.9	50	AAI23191
16	22	81.5	22	AAQ14244
17	22	81.5	22	AAQ62302
18	22	81.5	22	AAI88787
19	22	81.5	22	AAI84198
20	22	81.5	22	AAI01841
21	22	81.5	22	AAV58784
22	19	70.4	70	AAV01832
23	18	66.7	69	AAV01831
24	17.4	64.4	23	AAQ86124
25	17.4	64.4	49	AAI35972
26	17	63.0	51	AAI37652
27	17	63.0	56	AAQ46949
28	17	63.0	68	AAV01830
29	16.4	60.7	28	AAI84608
30	16.4	60.7	65	AAI38971
31	16	59.3	67	AAQ51057
32	15.8	58.5	20	AAI34614
33	15.8	58.5	60	AAI36106
34	15.8	58.5	65	AAI36239
35	15.8	58.5	90	AAI36239
36	15.6	57.8	60	AAI35411
37	15.6	57.8	80	AAI32363
38	15.4	56.3	38	AAI38971
39	15.2	56.3	29	AAI38971
40	15.2	56.3	29	AAI4336
41	15.2	56.3	51	AAI79619
42	15.2	56.3	60	AAI37050
43	15	55.6	18	AAI91968
44	15	55.6	20	AAI39479
45	15	55.6	21	AAI91680

ALIGNMENTS

RESULT 1
AAZ60859/c
AAZ60859 standard; DNA: 27 BP.

16-MAY-2000 (first entry)

Oligonucleotide used to detect bcr b3-abl fusion transcripts.

Fusion transcript; translocation; bcr b3 region; abl gene;
amplification assay; detection assay; medical diagnosis;
clinical monitoring; chimeric RNA; fusion RNA; condition marker;
disease marker; cancer; leukemia; ss.

Synthetic.

WO200005418-A1

03-FEB-2000.

23-JUL-1999; 99WO-US16632.

23-JUL-1996; 98US-0121239.

(GENE) GEN-PROBE INC.

Harvey RC, Eastman, PS.

WPI; 2000-182736/16.

Novel methods for preparing RNA from biological samples, used for the

Human bcr-abl onco
CML chromosomal tr
CML-2 chromosomal
CML-2 chromosomal
CML chromosomal tr
Primer CML1. SYN
PCR primer for amp
Leukemic cell BCR
PCR primer reverse PC
PCR primer ab150 u
Detection probe to
Asymmetric hammer
Asymmetric hammer
bcr-abl mRNA junct
Human Ras GTP enzy
Human SNP flanking
Branched probe to
Asymmetric hammer
Primer for AML1-MT
Mouse spliced tran
Asymmetric hammer
Human glucokinase
Human spliced tran
Mouse spliced tran
HIV DNA encoding G
Human spliced tran
Artificial NS4 mos
Human C12A1 gene e
Interleukin IL-3
Human DNA contain
Human spliced tran
RNA sequence disc
Chronic myelogenous
PCR primer for bcr

PT detection and measurement of nucleic acids and fusion nucleic acids -
XX Claim 19; Page 43; 49pp; English.
XX
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
Db 27 TCTGACTTTGAGCCTCAGGCTCTGAGT 1

RESULT 2
AAZ60860/c
ID AAZ60860 standard; RNA; 27 BP.

XX AAZ60860;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KM clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX disease marker; cancer; leukemia; ss.

OS Synthetic.

XX WO200005418-A1.

PN 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids -
XX Claim 19; Page 43; 49pp; English.
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 U; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
Db 27 TCTGACTTTGAGCCTCAGGCTCTGAGT 1

RESULT 3
AAZ60861
ID AAZ60861 standard; DNA; 27 BP.

XX AAZ60861;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KM clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX disease marker; cancer; leukemia; ss.

OS Synthetic.

XX WO200005418-A1.

PN 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids -
XX Claim 19; Page 43; 49pp; English.
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes
XX a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is
XX used for the simple and rapid preparation of RNA from a biological

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SO Sequence 27 BP; 4 A; 6 C; 8 G; 9 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCTCAGGCTGTGAGT 27
Db 1 TCTGACTTTGAGCTCAGGCTGTGAGT 27

RESULT 4

AAZ60862 ID AAZ60862 standard; RNA; 27 BP.

AC AAZ60862;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

WPI: 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the
detection and measurement of nucleic acids and fusion nucleic acids -

Claim 19; Page 44; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
the invention to detect fusion transcripts produced from a translocation
between the bcr b3 region and the abl gene. The specification describes
a method for detecting a fusion nucleic acid (particularly chimeric RNA
species), in a biological sample. The method comprises contacting a
sample of fusion nucleic acid with primers, amplifying the hybridized
fusion nucleic acid, and detecting the target hybrid. The method is
used for the sample and rapid preparation of RNA from a biological
sample, particularly from the cytoplasm of eukaryotic cells, which is
suitable for use in an amplification and detection assay. The methods
are used for the analysis and detection of nucleic acids in biological
samples. The methods are useful in the human medical and veterinary
fields, for medical diagnoses and clinical monitoring of a patient's
response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SO Sequence 27 BP; 4 A; 6 C; 8 G; 9 U; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCTCAGGCTGTGAGT 27
Db 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27

RESULT 5

AAZ60840/C ID AAZ60840 standard; DNA; 54 BP.

AC AAZ60840;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

WPI: 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the
detection and measurement of nucleic acids and fusion nucleic acids -

Claim 19; Page 39; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
the invention to detect fusion transcripts produced from a translocation
between the bcr b3 region and the abl gene. The specification describes
a method for detecting a fusion nucleic acid (particularly chimeric RNA
species), in a biological sample. The method comprises contacting a
sample of fusion nucleic acid with primers, amplifying the hybridized
fusion nucleic acid, and detecting the target hybrid. The method is
used for the sample and rapid preparation of RNA from a biological
sample, particularly from the cytoplasm of eukaryotic cells, which is
suitable for use in an amplification and detection assay. The methods
are used for the analysis and detection of nucleic acids in biological
samples. The methods are useful in the human medical and veterinary
fields, for medical diagnoses and clinical monitoring of a patient's
response to therapy where a disease or medical condition is associated
with a particular type and/or level of mRNA present in the sample. The
methods are also useful for detecting or quantifying fusion or chimeric
RNA species, and for detecting a translocation as a marker for a given
condition or disease, e.g. translocations associate with cancers,
particularly forms of leukemia.

SO Sequence 54 BP; 20 A; 12 C; 11 G; 11 T; 0 other;
 Query Match 100.0%; Score 27; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 |||||
 DB 54 TCTGACTTTGAGCCTCAGGCTGTGAGT 28

RESULT 6
 AAZ60841/C
 ID AAZ60841 standard; RNA; 54 BP.

AC AAZ60841;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;
 amplification assay; detection assay; medical diagnosis;
 clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

WPI; 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids -

Claim 19; Page 40; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for the analysis and detection of nucleic acids in biological samples. The methods are useful in the human medical and veterinary fields, for medical diagnoses and clinical monitoring of a patient's response to therapy where a disease or medical condition is associated with a particular type and/or level of mRNA present in the sample. The methods are also useful for detecting or quantifying fusion or chimeric RNA species, and for detecting a translocation as a marker for a given condition or disease, e.g. translocations associate with cancers, particularly forms of leukemia.

Sequence 54 BP; 20 A; 12 C; 11 G; 11 U; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 |||||
 DB 54 TCTGACTTTGAGCCTCAGGCTGTGAGT 28

RESULT 7
 AAZ60842
 ID AAZ60842 standard; DNA; 54 BP.

AC AAZ60842;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;
 amplification assay; detection assay; medical diagnosis;
 clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

WPI; 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids -

Claim 19; Page 40; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for the analysis and detection of nucleic acids in biological samples. The methods are useful in the human medical and veterinary fields, for medical diagnoses and clinical monitoring of a patient's response to therapy where a disease or medical condition is associated with a particular type and/or level of mRNA present in the sample. The methods are also useful for detecting or quantifying fusion or chimeric RNA species, and for detecting a translocation as a marker for a given condition or disease, e.g. translocations associate with cancers, particularly forms of leukemia.

Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 |||||
 DB 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27

RESULT 8

AAZ60843
ID AAZ60843 standard; RNA; 54 BP.
XX
AC AAZ60843;
XX
XX 16-MAY-2000 (first entry)
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
OS Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US16832.
XX
XX 23-JUL-1998; 98US-0121239.
XX (GENP) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 40; 49pp; English.
XX
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes
XX a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is
XX used for the simple and rapid preparation of RNA from a biological
XX sample, particularly from the cytoplasm of eukaryotic cells, which is
XX suitable for use in an amplification and detection assay. The methods
XX are used for the analysis and detection of nucleic acids in biological
XX fields, for medical diagnoses and clinical monitoring of a patients
XX response to therapy where a disease or medical condition is associated
XX with a particular type and/or level of mRNA present in the sample. The
XX methods are also useful for detecting or quantifying fusion or chimeric
XX RNA species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia.
XX
XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 U; 0 other;
XX
XX Query Match 100.0%; Score 27; DB 21; Length 54;
XX Best Local Similarity 66.7%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
XX Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
XX :|||||:|||||:|||||:|||||:
XX 1 UCUGACUUGAGCCUCACGAGGUCUGAGU 27
XX
XX RESULT 9
XX AAO34631
XX ID AAO34631 standard; cDNA; 80 BP.
XX AC AAO34631;
XX XX
XX 10-MAY-1993 (first entry)
XX

XX
DE Human Ph1-positive cell line bcr-abl junction.
XX
XX Leukemia; treatment; blast crisis; specific; CML; translocation;
XX Philadelphia chromosome; chronic myeloid; chronic myelogenous;
XX leukemia; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Key 33..40
XX misc_feature /tag= a
XX /note= "bcr-abl breakpoint"
XX misc_feature 31..32
XX /tag= b
XX /note= "breakpoint junction target sequence"
XX
XX WO9222303-A.
XX
XX 23-DEC-1992.
XX
XX 15-JUN-1992; 92WO-US05035.
XX
XX 18-JUN-1991; 91US-0718302.
XX 14-APR-1992; 92US-0869911.
XX
XX (UTEM) UNIV TEMPLE.
XX
XX Calabretta B, Gewirtz AM;
XX
XX WPI; 1993-017893/02.
XX
XX Treating Ph1-positive leukemia(s) using bcr-abl anti-sense oligo-
XX nucleotide(s) - to selectively inhibit leukemic cell proliferation
XX without adversely affecting normal hematopoiesis
XX
XX Disclosure; Fig 5; 74pp; English.
XX
XX This is the sequence around the bcr-abl junction derived from the
XX cells of a Ph1 positive cell line. The bcr derived portion of the
XX sequence lies upstream from the breakpoint. The junction is formed
XX by the fusion of bcr exon 1 to c-abl exon 2.
XX
XX Sequence 80 BP; 16 A; 22 C; 27 G; 15 T; 0 other;
XX
XX Query Match 96.3%; Score 26; DB 14; Length 80;
XX Best Local Similarity 100.0%; Pred. No. 0.042;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
XX :|||||:|||||:|||||:|||||:
XX 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80
XX
XX RESULT 10
XX AAV20460
XX ID AAV20460 standard; DNA; 80 BP.
XX AC AAV20460;
XX XX
XX 17-JUN-1998 (first entry)
XX
XX Human bcr-abl oncogene b1a2 genotype.
XX
XX Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
XX cancer; antisense oligonucleotide; bcr-abl; ds.
XX
XX Homo sapiens.
XX
XX US5734039-A.
XX 31-MAR-1998.
XX
XX

PF 15-SEP-1994; 94US-0306691.
 XX
 PR 15-SEP-1994; 94US-0306691.
 XX
 PA (UYJE-) UNTV JEFFERSON THOMAS.
 XX
 PI Calabretta B, Skorski T;
 XX
 DR WPI; 1998-229882/20.
 XX
 PT Anticancer composition comprising two anti-sense oligo:nucleotide(s)
 XX - targeting cytoplasmic and nuclear oncogene(s)
 XX
 PS Claim 1: Column 109-110; 92pp; English.
 XX
 CC The present sequence represents an oncogene from the present invention.
 CC The present invention describes a composition which comprises two
 CC antisense oligonucleotides. The first oligonucleotide is specific for a
 CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1,
 CC c-fms, c-fos, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and
 CC c-yes. The second oligonucleotide is specific for a nuclear oncogene or
 CC proto-oncogene selected from myc, jun, c-ets, c-fos, c-myc, B-myc,
 CC c-rel, c-vav, c-ski, c-spl, cyclin D1, PML/RAR alpha, AML1/MF8,
 CC E2A/p1 and ALL-1/AF-4. The composition is used for treating cancer.
 CC The combination of antisense oligonucleotides has synergistically
 CC enhanced ability to inhibit growth of cancer cells.
 CC
 XX
 SO Sequence 80 BP; 16 A; 22 C; 27 G; 15 T; 0 other;
 XX
 Query Match 96.3%; Score 26; DB 19; Length 80;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
 Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80
 XX
 RESULT 11
 ID AA086626/c
 AC AA086626 standard; DNA; 50 BP.
 XX
 AC AA086626;
 XX
 DT 15-NOV-1995 (first entry)
 XX
 DE CML chromosomal translocation minus strand primer.
 OS Primer; autocatalytic; target; CML; translocation; ss.
 XX
 OS Synthetic.
 XX
 PN US5399491-A.
 PD 21-MAR-1995.
 XX
 PF 11-JUL-1989; 89US-0379501.
 XX
 PR 11-JUL-1989; 89US-0379501.
 PR 10-JUL-1990; 90US-0550837.
 PR 19-MAR-1992; 92US-0855732.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 DR WPI; 1995-130686/17.
 XX
 PT Amplification of nucleic acid targets - using a reverse
 PT transcriptase with RNase H activity and a RNA polymerase at
 PT constant temp.
 XX
 PS Disclosure; Column 9; 58pp; English.

XX
 CC AA086626-28 are primers and a probe for the CML chromosomal
 CC translocation. They are used to produce autocatalytic
 CC oligonucleotides which require no change in the experimental
 CC conditions i.e. constant temperature, pH and ionic strength.
 CC These sequences are useful in generating multiple copies of
 CC specific nucleic acid target sequences.
 CC
 XX
 SO Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;
 XX
 Query Match 88.9%; Score 24; DB 16; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 GACTTTGAGCCTCAGGCTCTGAGT 27
 Db 50 GACTTTGAGCCTCAGGCTCTGAGT 27
 XX
 RESULT 12
 ID AAT42417/c
 AC AAT42417 standard; DNA; 50 BP.
 XX
 AC AAT42417;
 XX
 DT 28-APR-1997 (first entry)
 XX
 DE CML chromosomal translocation primer #1.
 XX
 KW HIV; probe; primer; amplify; polymerase chain reaction; microorganism;
 KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
 XX
 OS Synthetic.
 XX
 PN BP731175-A2.
 PD 11-SEP-1996.
 XX
 PF 10-JUL-1990; 90EP-0307503.
 XX
 PR 11-JUL-1989; 89US-0379501.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI McDonough S;
 XX
 DR WPI; 1996-403995/41.
 XX
 PT Detection of HIV nucleic acids in samples - using new specific
 PT oligo-nucleotide(s) for the amplification and detection of target
 PT sequences.
 XX
 PS Disclosure; Page 8; 66pp; English.
 XX
 CC AAT42417-T42419 represent primers and a probe for the CML chromosomal
 CC translocation t(9;22). These sequences can be used in modified versions
 CC of the kits of the invention. The kits of the invention are for
 CC detecting the presence of HIV nucleic acid sequences in a sample. The
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),
 CC and a probe (such as AAT42404) for detection of the amplified sequence.
 CC By using these sequences, the amplification of HIV nucleic acid sequences
 CC is improved. The kits can also be used for the detection of other
 CC microorganisms, by using different probe sequences. Other sequences
 CC that can be detected using this method include those from HBV (using the
 CC sequences shown in AAT42410-T42412) and BCL-2 (using AAT42413-T42416).
 CC The samples can be clinical, environmental or forensic samples, and the
 CC method produces large amounts of the target sequence for a variety of
 CC uses. The method can also be used to produce multiple copies of a
 CC target sequence for use in cloning, and sequencing, and to produce probes
 CC for the target sequence.
 CC
 XX
 SO Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 88.9%; Score 24; DB 17; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGCTGAGT 27
|||||
DB 50 GACTTGGAGCCTCAGGCTGAGT 27

RESULT 13

AAAT15571/C
ID AAT15571 standard; DNA; 50 BP.

AC AAT15571;

DT 17-JUL-1996 (first entry)

DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.

KW CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
auto-catalytic; synthesis; RNA target sequence; assay; detection;
quantification; ss.

OS Synthetic.

PN US5480784-A.

PD 02-JAN-1996.

PP 11-JUL-1989; 89US-0379501.

PR 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

PA (GENP-) GEN-PROBE INC.

PI Fultz TJ, Kacian DL;

WPI: 1996-068248/07.

PT Auto-catalytic synthesis of multiple copies of an RNA target
sequence - uses cooperative action of a DNA and RNA polymerase in
presence of RNase H, useful for detection of target sequence e.g. in
clinical or environmental sample

PS Example; Columns 9-10; 51pp; English.

CC The present sequence is a primer for the CML-2 chromosomal
translocation major breakpoint t(9;22), which was used to
demonstrate an improved method for synthesising multiple copies of
a RNA target sequence. The method comprises combining the target
with a primer which hybridises to the 3'-terminal portion of the
target, a promoter primer which hybridises with a portion of the
DNA primer extension prod., reverse transcriptase, RNase H and
transcriptase. It can be used as a component of an assay to detect
and/or quantitate specific target sequences in clinical,
environmental or forensic samples. It also has the advantages of
being autocatalytic, using the cooperative action of a DNA
polymerase e.g. a reverse transcriptase and avoids repetitive
manipulations of reaction conditions, e.g. temp., ionic strength
and pH.

SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 88.9%; Score 24; DB 17; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGCTGAGT 27
|||||
DB 50 GACTTGGAGCCTCAGGCTGAGT 27

RESULT 14
AAV6349/C
ID AAV6349 standard; DNA; 50 BP.

AC AAV6349;

DT 06-JAN-1999 (first entry)

DE CML-2 chromosomal translocation t(9;22) primer.

KW CML-2 chromosomal translocation t(9;22); block splice template;
autocatalytic RNA amplification; primer; ss.

OS Synthetic.

PN US5824518-A.

PD 20-OCT-1998.

PP 06-JUN-1995; 95US-0469067.

PR 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

PR 06-JUN-1995; 95US-0469067.

PA (GENP-) GEN-PROBE INC.

PI Fultz TJ, Kacian DL;

WPI: 1998-582557/49.

PT Block splice template useful for amplification of nucleic acids -
comprises two nucleic acid regions, the first region located 3' of
the second region and blocked at its 3' terminus to inhibit primer
extension by a DNA polymerase

PS Example 15; Column 9; 51pp; English.

CC AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,
for the (+) and (-) strands respectively. The primers are used to
describe the invention, together with probe AAV6351. The specification
describes methods of synthesising multiple copies of a target nucleic
acid sequence autocatalytically under conditions of substantially
constant temperature, ionic strength and pH are provided in which
multiple RNA copies of the target sequence autocatalytically
generate additional copies. The target sequence is a block splice
template which comprises two nucleic acid regions. The first region is
located 3' of the second region and is blocked at its 3' terminus to
inhibit primer extension by a DNA polymerase, and the second region
comprises a promoter sequence recognised by an RNA polymerase. The
methods are used to amplify nucleic acids, especially RNA, for
analysis, cloning or probe production.

SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 88.9%; Score 24; DB 19; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGCTGAGT 27
|||||
DB 50 GACTTGGAGCCTCAGGCTGAGT 27

RESULT 15

AAZ23191/C
ID AAZ23191 standard; DNA; 50 BP.

AC AAZ23191;

DT 11-JUN-1999 (first entry)

DE CML chromosomal translocation t(9;22) primer #1.

XX Autocatalytic amplification; transcription-based amplification; CMU;
 KW thermalcycling; diagnostic; environmental testing; probe; detection;
 KW genetic disease; infectious disease; microorganism; food; forensic;
 KW paternity; primer; ss.

OS Synthetic.

PN US5888779-A.

PD 30-MAR-1999.

PF 05-JUN-1995; 95US-0461654.

PR 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

PR 05-JUN-1995; 95US-0461654.

(GENP-) GEN-PROBE INC.

Fultz TJ, Kacian DL;

WPI; 1999-253231/21.

Kit for autocatalytic amplification of RNA targets

Disclosure; Column 9; 51pp; English.

This invention describes a novel method for the autocatalytic amplification of an RNA target in a transcription-based amplification system without thermalcycling. The method generates oligonucleotides for diagnostic or environmental testing, for use e.g. as probes and in cloning. Typical applications are the detection of genetic or infectious diseases, the monitoring of responses to therapy, the quantitation or detection of microorganisms in foods, forensic studies and the establishment of paternity. Kits containing the products of the invention provide many copies of selected RNA targets under conditions of constant temperature, ionic strength and pH. Specific amplification of RNA targets increases sensitivity, convenience, accuracy and the reliability of assays.

Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match

88.9%; Score 24; DB 20; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 GACTTGAGCCTCAGGCTGAGT 27

50 GACTTGAGCCTCAGGCTGAGT 27

Search completed: December 21, 2002, 11:54:42
 Job time : 94.6816 secs

us-09-121-239-23.rng

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Run on: December 21, 2002, 02:00:32 ; Search time 92.6816 Seconds
(without alignments)
656.052 Million cell updates/sec

Sequence: 1 UCUGACUUUGAGCCUCAGGGUCUGAGU 27

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0
Maximum DB seq length: 100

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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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3	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1582.DAT.*
4	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1583.DAT.*
5	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1584.DAT.*
6	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1585.DAT.*
7	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1587.DAT.*
8	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1588.DAT.*
9	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1589.DAT.*
10	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1590.DAT.*
11	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1591.DAT.*
12	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1592.DAT.*
13	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1593.DAT.*
14	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1594.DAT.*
15	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1595.DAT.*
16	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1596.DAT.*
17	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1597.DAT.*
18	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1598.DAT.*
19	/SID52/gcgatata/geneseq/geneseqn-emb1/NA1599.DAT.*
20	/SID52/gcgatata/geneseq/geneseqn-emb1/NA2000.DAT.*
21	/SID52/gcgatata/geneseq/geneseqn-emb1/NA2001A.DAT.*
22	/SID52/gcgatata/geneseq/geneseqn-emb1/NA2001B.DAT.*
23	/SID52/gcgatata/geneseq/geneseqn-emb1/NA2001C.DAT.*
24	/SID52/gcgatata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	27	100.0	27	21	AA60859	Oligonucleotide us
c 2	27	100.0	27	21	AA60860	Oligonucleotide us
c 3	27	100.0	27	21	AA60861	Oligonucleotide us
c 4	27	100.0	27	21	AA60862	Oligonucleotide us
c 5	27	100.0	54	21	AA60840	Oligonucleotide us
c 6	27	100.0	54	21	AA60841	Oligonucleotide us
c 7	27	100.0	54	21	AA60842	Oligonucleotide us
c 8	27	100.0	54	21	AA60843	Oligonucleotide us
c 9	26	96.3	80	14	AA034631	Human Pfl-positive

C	10	26	96.3	80	19	AA20460
C	11	24	88.9	50	16	AA06626
C	12	24	88.9	50	17	AA74241
C	13	24	88.9	50	17	AA74241
C	14	24	88.9	50	19	AAV6349
C	15	24	88.9	50	20	AAV6349
C	16	22	81.5	22	12	AA04242
C	17	22	81.5	22	12	AA06230
C	18	22	81.5	22	18	AAV6878
C	19	22	81.5	22	24	ABN8419
C	20	22	74.1	50	19	AAV0184
C	21	19	70.4	24	19	AAV5878
C	22	19	70.4	70	19	AAV0182
C	23	18	66.7	69	19	AAV0181
C	24	17.4	64.4	23	16	AA06164
C	25	17.4	64.4	49	24	AAV5972
C	26	17	63.0	51	22	AAH3762
C	27	17	63.0	56	14	AAQ4694
C	28	16.4	60.7	68	19	AAV0180
C	29	16.4	60.7	65	20	AAH3468
C	30	15.4	58.5	28	24	AAH3468
C	31	15.4	58.5	27	19	AAV0182
C	32	15.8	58.5	20	14	AAO5105
C	33	15.8	58.5	60	24	ABN5461
C	34	15.8	58.5	65	24	ABN5461
C	35	15.8	58.5	90	24	ABN3623
C	36	15.6	57.8	90	24	ABN3541
C	37	15.6	57.8	80	20	AAH3236
C	38	15.4	57.8	38	24	AAH5824
C	39	15.2	55.3	29	17	AA71897
C	40	15.2	55.3	29	24	ABK1433
C	41	15.2	55.3	51	22	AAH7961
C	42	15.2	55.3	60	24	AAH7961
C	43	15	55.6	16	18	AAH9195
C	44	15	55.6	21	18	AAH9195
C	45	15	55.6	21	21	AAZ9180

XX	RESULT 1
XX	AA60859/c
ID	AA60859 standard; DNA; 27 BP.
XX	
AC	AA60859;
XX	
DT	16-MAY-2000 (first entry)
DE	Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX	
KW	Fusion transcript; translocation; bcr b3 region; abl gene;
KW	amplification assay; detection assay; medical diagnosis; marker;
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX	disease marker; cancer; leukemia; ss.
XX	
OS	Synthetic.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
PE	23-JUL-1999; 99WD-0516832.
XX	
PR	23-JUL-1998; 98US-0712139.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Harvey RC, Eastman PS;
DR	WPI; 2000-182730/16.
XX	
TX	Novel methods for preparing RNA from biological samples, used for the

PT detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 43; 49pp; English.
XX
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patients
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
Db 27 TCTGACTTGTGAGCCTCAGGCTCGAGT 1
:|||||:|||||:|||||:|||||:|||||

RESULT 2

AAZ60860/C
ID AAZ60860 standard; RNA; 27 BP.

AC AAZ60860;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 43; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patients
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 U; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
Db 27 TCTGACTTGTGAGCCTCAGGCTCGAGT 1
:|||||:|||||:|||||:|||||:|||||

RESULT 3

AAZ60861
ID AAZ60861 standard; DNA; 27 BP.

AC AAZ60861;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 43; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological

AAZ60843
 ID AAZ60843 standard; RNA; 54 BP.
 XX
 AC AAZ60843;
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 XX
 KW Fusion transcript; translocation: bcr b3 region: abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO200005418-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 23-JUL-1999; 99WO-US16832.
 XX
 PR 23-JUL-1998; 98US-0121239.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Harvey RC, Eastman PS;
 XX
 DR WPI: 2000-182730/16.
 XX
 PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids -
 XX
 PS Claim 19; Page 40; 49pp; English.
 XX
 SS Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC method are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 U; 0 other;
 XX
 SO
 XX
 Query Match 100.0%; Score 27; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 UCUGACUUGAGCCUCACAGGUGUCGAGU 27
 DB 1 UCUGACUUGAGCCUCACAGGUGUCGAGU 27
 XX
 RESULT 9
 ID AAZ60843 standard; RNA; 80 BP.
 XX
 AC AAZ60843;
 XX
 DT 10-MAY-1993 (first entry)

XX
 DE Human Ph1-positive cell line bcr-abl junction.
 XX
 KW Leukemia; treatment; blast crisis; specific; CML; translocation;
 KW Philadelphia chromosome; chronic myeloid; chronic myelogenous;
 KW leukemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO9222303-A.
 XX
 PD 23-DEC-1992.
 XX
 PF 15-JUN-1992; 92MO-US05035.
 XX
 PR 18-JUN-1991; 91US-0718302.
 XX
 PR 14-APR-1992; 92US-0869911.
 XX
 PA (UTEM) UNIV TEMPLE.
 XX
 PI Calabretta B, Gewirtz AM;
 XX
 DR WPI: 1993-017893/02.
 XX
 PT Treating Ph1-positive leukemia(s) using bcr-abl anti-sense oligo-
 PT nucleotide(s) - to selectively inhibit leukemic cell proliferation
 PT without adversely affecting normal hematopoiesis
 XX
 PS Disclosure; Fig 5; 74pp; English.
 XX
 CC This is the sequence around the bcr-abl junction derived from the
 CC cells of a Ph1 positive cell line. The bcr derived portion of the
 CC sequence lies upstream from the breakpoint. The junction is formed
 CC by the fusion of bcr exon 1 to c-abl exon 2.
 CC
 XX Sequence 80 BP; 16 A; 22 C; 27 G; 15 T; 0 other;
 XX
 SO
 XX
 Query Match 96.3%; Score 26; DB 14; Length 80;
 Best Local Similarity 69.2%; Pred. No. 0.042;
 Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 OY 1 UCUGACUUGAGCCUCACAGGUGUCGAG 26
 DB 55 TCTGACTTGAGCCTCAGGGGTCTGAG 80
 XX
 RESULT 10
 ID AAV20460 standard; DNA; 80 BP.
 XX
 AC AAV20460;
 XX
 DT 17-JUN-1998 (first entry)
 XX
 DE Human bcr-abl oncogene b1a2 genotype.
 XX
 KW Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
 KW cancer; antisense oligonucleotide; bcr-abl; ds.
 XX
 OS Homo sapiens.
 XX
 PN US5734039-A.
 XX
 PD 31-MAR-1998.
 XX

PF	15-SEP-1994;	94US-0306691.
XX		
PR	15-SEP-1994;	94US-0306691.
XX		
PA	(UYJE-) UNIV JEFFERSON THOMAS.	
XX		
PI	Calabretta B, Skorski T;	
XX		
DR	WPI; 1998-229882/20.	
XX		
PT	Anticancer composition comprising two anti-sense oligo:nucleotide(s)	
PT	- targetting cytoplasmic and nuclear oncogene(s)	
XX		
PS	Claim 1; Column 109-110; 92pp; English.	
XX		

CC The present sequence represents an oncogene from the present invention.
 CC The present invention describes a composition which comprises two
 CC antisense oligonucleotides. The first oligonucleotide is specific for a
 CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, Bcr-1,
 CC c-fms, c-tos, c-klt, c-met, c-trk, c-src, c-abl, bcr-abl, c-grf and
 CC c-yes. The second oligonucleotide is specific for a nuclear oncogene or
 CC proto-oncogene selected from myc, jun, c-ets, c-tos, c-myb, B-myd,
 CC c-rel, c-vav, c-eki, c-spi, cyclin D1, PML/RAR alpha, AML1/MTG8,
 CC E2A/p1 and AL1-1/AF-4. The composition is used for treating cancer.
 CC The combination of antisense oligonucleotides has synergistically
 CC enhanced ability to inhibit growth of cancer cells.
 CC
 CC
 CC Sequence 80 BP; 16 A; 22 C; 27 G; 15 T; 0 other;

Query Match	96.3%;	Score 26;	DB 19;	Length 80;
Best Local Similarity	69.2%;	Pred. No. 0.042;		
Matches 18; Conservative	8;	Mismatches 0;	Indels 0;	Gaps 0

DY **1** UCUGACUUUGAGCCCTCAGGGUCUAG 26
 |:|:::|||||:|||||:|:
Db **55** TCTGACTTTGAGCCTCAGGGTCTGAG 80

RESULT 11

ID	AAQ86626	standard; DNA; 50 BP.
XX	AAQ86626/c	

AC AAQ86626;

DT 15-NOV-1995 (first entry)
YY

CML chromosomal translocation minus strand primer.

primer; autocatalytic; target; CML; translocation; ss.

XX 00
cymuicellc

XX

XX

XX

PR 10-JUL-1990; 90US-0550837.

XX (CENB-) CEN-DPOBF TWO

Fuller, T. T. Kacian DL:

WPI: 1995-130686/17

	Amplification of nucleic acids
PT	
.....	

PT constant temp.

PS Disclosure; Column 9; 58pp; English.

XX AAO86656-28 are primers and a probe for the CML chromosomal
CC translocation. They are used to produce autocatalytic
CC oligonucleotides which require no change in the experimental
CC conditions i.e. constant temperature, pH and ionic strength.
CC These sequences are useful in generating multiple copies of
CC specific nucleic acid target sequences.
XX
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other:

Query Match	88.9%	Score 24	DB 16	Length 50
Best Local Similarity	70.8%	Pred No. 0.3		
Matches 17; Conservative	7	Mismatches	0	Gaps 0

QY 4 GACUUGAGCCUCAGGGUCUGAGU 27
|||::|||::|||::|||::|||::
Db 50 GACTTGAGCCTCAGGGTCTGAGT 27

RESULT 12

ID	standard; DNA; 50 BP.
AA142417	

AA142417
AC
XX

DI 28-APR-199/ (first entry)
XX

CMC chromosomal translocation primer #1.

PCR; hepatitis B virus: HBV: CMT: SS: BCL-2; polymerase chain reaction; microorganism; KM

05 Synthetic.

PN EP731175-A2.

PD 11-SEP-1996

PF 10-JUL-1990; 90EP-0307503
VY

PK	11-JUL-1989;	89US-0379501.
XX		

PA (GENP-) GEN-PROBE INC.
XX XX

McDonough, S;
XX
XX

[illegible]

PT oligo-nucleotide(s) for the amplification and detection of target

XX

33XX

AAV4741-T92419 represent primers and a probe for the CMV chromosomal translocation t(9;22). These sequences can be used in modified versions of the kits of the invention. The kits of the invention, are for detecting the presence of HIV nucleic acid sequences in a sample. The kits comprise two amplification primers (such as AAT40182 and AAT40183), and a probe (such as AAT42404) for detection of the amplified sequence. By using these sequences, the amplification of HIV nucleic acid sequences is improved. The kits can also be used for the detection of other microorganisms, by using different probe sequences. Other sequences that can be detected using this method include those from HBV (using the sequences shown in AAT44410-T92412), and BCL-2 (using AAT42413-T92416). The samples can be clinical, environmental or forensic samples, and the method produces large amounts of the target sequence for a variety of uses. The method can also be used to produce multiple copies of a target sequence for use in cloning, and sequencing, and to produce probes for the target sequence.

50 Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

```

Query Match      88.9%; Score 24; DB 17; Length 50;
Best Local Similarity 70.8%; Pred. No. 0.3;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUUGAGCCUCAGGUCUGAGU 27
DB 50 GACUUGAGCCUCAGGUCUGAGU 27

RESULT 13
AAT15571/c
ID AAT15571 standard; DNA; 50 BP.
AC AAT15571;
AT 17-JUL-1996 (first entry)
DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
XX CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
XX auto-catalytic; synthesis; RNA target sequence; assay; detection;
XX quantification; ss.
OS Synthetic.
XX US5480784-A.
XX 02-JAN-1996.
XX 11-JUL-1989; 89US-0379501.
XX 10-JUL-1990; 90US-0550837.
XX 11-JUL-1989; 89US-0379501.
XX (GENP-) GEN-PROBE INC.
XX Fultz TJ, Kacian DL;
XX WPI; 1996-068248/07.
XX
XX Auto-catalytic synthesis of multiple copies of an RNA target
XX sequence - uses cooperative action of a DNA and RNA polymerase in
XX presence of RNase H, useful for detection of target sequence e.g. in
XX clinical or environmental sample
XX
XX Example; Columns 9-10; 51bp; English.
XX
XX The present sequence is a primer for the CML-2 chromosomal
XX translocation major breakpoint t(9;22), which was used to
XX demonstrate an improved method for synthesizing multiple copies of
XX a RNA target sequence. The method comprises combining the target
XX with a primer which hybridises to the 3'-terminal portion of the
XX target, a promoter primer which hybridises with a portion of the
XX DNA primer extension prod., reverse transcriptase, RNase H and
XX transcriptase. It can be used as a component of an assay to detect
XX and/or quantitate specific target sequences in clinical,
XX environmental or forensic samples. It also has the advantages of
XX being autocatalytic, using the cooperative action of a DNA
XX polymerase, e.g. a reverse transcriptase and avoids repetitive
XX manipulations of reaction conditions, e.g. temp., ionic strength
XX and pH.
XX
XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match      88.9%; Score 24; DB 17; Length 50;
Best Local Similarity 70.8%; Pred. No. 0.3;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUUGAGCCUCAGGUCUGAGU 27
DB 50 GACUUGAGCCUCAGGUCUGAGU 27

RESULT 13
AAT15571/c
ID AAT15571 standard; DNA; 50 BP.
AC AAT15571;
AT 17-JUL-1996 (first entry)
DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
XX CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
XX auto-catalytic; synthesis; RNA target sequence; assay; detection;
XX quantification; ss.
OS Synthetic.
XX US5480784-A.
XX 02-JAN-1996.
XX 11-JUL-1989; 89US-0379501.
XX 10-JUL-1990; 90US-0550837.
XX 11-JUL-1989; 89US-0379501.
XX (GENP-) GEN-PROBE INC.
XX Fultz TJ, Kacian DL;
XX WPI; 1996-068248/07.
XX
XX Auto-catalytic synthesis of multiple copies of an RNA target
XX sequence - uses cooperative action of a DNA and RNA polymerase in
XX presence of RNase H, useful for detection of target sequence e.g. in
XX clinical or environmental sample
XX
XX Example; Columns 9-10; 51bp; English.
XX
XX The present sequence is a primer for the CML-2 chromosomal
XX translocation major breakpoint t(9;22), which was used to
XX demonstrate an improved method for synthesizing multiple copies of
XX a RNA target sequence. The method comprises combining the target
XX with a primer which hybridises to the 3'-terminal portion of the
XX target, a promoter primer which hybridises with a portion of the
XX DNA primer extension prod., reverse transcriptase, RNase H and
XX transcriptase. It can be used as a component of an assay to detect
XX and/or quantitate specific target sequences in clinical,
XX environmental or forensic samples. It also has the advantages of
XX being autocatalytic, using the cooperative action of a DNA
XX polymerase, e.g. a reverse transcriptase and avoids repetitive
XX manipulations of reaction conditions, e.g. temp., ionic strength
XX and pH.
XX
XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match      88.9%; Score 24; DB 19; Length 50;
Best Local Similarity 70.8%; Pred. No. 0.3;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUUGAGCCUCAGGUCUGAGU 27
DB 50 GACUUGAGCCUCAGGUCUGAGU 27

RESULT 14
AAV6349/c
ID AAV6349 standard; DNA; 50 BP.
AC AAV6349;
AT 06-JAN-1999 (first entry)
DE CML-2 chromosomal translocation t(9;22) primer.
XX CML-2 chromosomal translocation t(9;22); block splice template;
XX autocatalytic RNA amplification; primer; ss.
OS Synthetic.
XX US5824518-A.
XX 20-OCT-1998.
XX 06-JUN-1995; 95US-0469067.
XX 10-JUL-1990; 90US-0550837.
XX 11-JUL-1989; 89US-0379501.
XX 06-JUN-1995; 95US-0469067.
XX (GENP-) GEN-PROBE INC.
XX Fultz TJ, Kacian DL;
XX WPI; 1998-582557/49.
XX
XX Block splice template useful for amplification of nucleic acids -
XX comprises two nucleic acid regions, the first region located 3' of
XX the second region and blocked at its 3' terminus to inhibit primer
XX extension by a DNA polymerase
XX
XX Example 15; Column 9; 51bp; English.
XX
XX AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,
XX for the (+) and (-) strands respectively. The primers are used to
XX exemplify the invention, together with probe AAV6351. The specification
XX describes methods of synthesizing multiple copies of a target nucleic
XX acid sequence autocatalytically under conditions of substantially
XX constant temperature, ionic strength and pH are provided in which
XX multiple RNA copies of the target sequence autocatalytically
XX generate additional copies. The target sequence is a block splice
XX template which comprises two nucleic acid regions. The first region is
XX located 3' of the second region and is blocked at its 3' terminus to
XX inhibit primer extension by a DNA polymerase, and the second region
XX comprises a promoter sequence recognised by an RNA polymerase. The
XX methods are used to amplify nucleic acids, especially RNA, for
XX analysis, cloning or probe production.
XX
XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match      88.9%; Score 24; DB 19; Length 50;
Best Local Similarity 70.8%; Pred. No. 0.3;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUUGAGCCUCAGGUCUGAGU 27
DB 50 GACUUGAGCCUCAGGUCUGAGU 27

RESULT 15
AAV6349/c
ID AAV6349 standard; DNA; 50 BP.
AC AAV6349;
AT 11-JUN-1999 (first entry)
DE CML chromosomal translocation t(9;22) primer #1.

```

XX Autocatalytic amplification; transcription-based amplification; CMV;
 KW thermalcycling; diagnostic; environmental testing; probe; detection;
 KW genetic disease; infectious disease; microorganism; food; forensic;
 KW paternity; primer; ss.

OS Synthetic.

PN US588779-A.

PD 30-MAR-1999.

PP 05-JUN-1995; 95US-0461654.

PR 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

PR 05-JUN-1995; 95US-0461654.

PA (GENP-) GEN-PROBE INC.

PI Fultz TJ, Kacian DL;

DR WPI; 1999-253231/21.

PT Kit for autocatalytic amplification of RNA targets

PS Disclosure; Column 9; Sipp; English.

CC This invention describes a novel method for the autocatalytic
 CC amplification of an RNA target in a transcription-based amplification
 CC system without thermalcycling. The method generates oligonucleotides for
 CC diagnostic or environmental testing, for use e.g. as probes and in
 CC cloning. Typical applications are the detection of genetic or infectious
 CC diseases, the monitoring of responses to therapy, the quantitation or
 CC detection of microorganisms in foods, forensic studies and the
 CC establishment of paternity. Kits containing the products of the invention
 CC provide many copies of selected RNA targets under conditions of constant
 CC temperature, ionic strength and pH. Specific amplification of RNA targets
 CC increases sensitivity, convenience, accuracy and the reliability of
 CC assays.

SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 88.9%; Score 24; DB 20; Length 50;

Best Local Similarity 70.8%; Pred. No. 0.3;

Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUUGAGCCUCAGGUCUGAGU 27

Db 50 GACTTGGAGCCTCAGGCTCTGAGT 27

Search completed: December 21, 2002, 11:54:43
 Job time : 93.6816 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 : Search time 82.3837 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-16
Perfect score: 24
Sequence: 1 GTGGAACATGAGCCCTTCAGCGC 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: N_Geneseq_101002.*
2: /SID2/gcgdata/geneseq/emb1/NA1980.DAT.*
3: /SID2/gcgdata/geneseq/emb1/NA1981.DAT.*
4: /SID2/gcgdata/geneseq/emb1/NA1982.DAT.*
5: /SID2/gcgdata/geneseq/emb1/NA1983.DAT.*
6: /SID2/gcgdata/geneseq/emb1/NA1984.DAT.*
7: /SID2/gcgdata/geneseq/emb1/NA1985.DAT.*
8: /SID2/gcgdata/geneseq/emb1/NA1986.DAT.*
9: /SID2/gcgdata/geneseq/emb1/NA1987.DAT.*
10: /SID2/gcgdata/geneseq/emb1/NA1988.DAT.*
11: /SID2/gcgdata/geneseq/emb1/NA1989.DAT.*
12: /SID2/gcgdata/geneseq/emb1/NA1990.DAT.*
13: /SID2/gcgdata/geneseq/emb1/NA1991.DAT.*
14: /SID2/gcgdata/geneseq/emb1/NA1992.DAT.*
15: /SID2/gcgdata/geneseq/emb1/NA1993.DAT.*
16: /SID2/gcgdata/geneseq/emb1/NA1994.DAT.*
17: /SID2/gcgdata/geneseq/emb1/NA1995.DAT.*
18: /SID2/gcgdata/geneseq/emb1/NA1996.DAT.*
19: /SID2/gcgdata/geneseq/emb1/NA1997.DAT.*
20: /SID2/gcgdata/geneseq/emb1/NA1998.DAT.*
21: /SID2/gcgdata/geneseq/emb1/NA1999.DAT.*
22: /SID2/gcgdata/geneseq/emb1/NA2000.DAT.*
23: /SID2/gcgdata/geneseq/emb1/NA2001.DAT.*
24: /SID2/gcgdata/geneseq/emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	100.0	24	AAZ60855
2	24	100.0	24	AAZ60856
3	24	100.0	24	AAZ60857
4	24	100.0	24	AAZ60858
5	17.2	71.7	60	ABN38552
6	17.2	71.7	65	ABN54940
7	15.8	65.8	56	AAO46947
8	15.8	65.8	60	ABN3790
9	15.6	65.0	35	AAA47720

C	10	15.6	65.0	35	22	AAZ16331	Human KOD delta (r
C	11	15.6	65.0	42	22	AAZ12048	Antisense oligonuc
C	12	15.6	65.0	95	22	ABAV3324	Human foetal liver
C	13	15.6	65.0	95	22	AAK21762	Human brain expres
C	14	15.6	65.0	95	22	AAK47927	Human bone marrow
C	15	15.6	65.0	95	22	AAI53756	Probe #22442 used
C	16	15.6	65.0	95	24	ABN21891	Human genome-deriv
C	17	15.4	64.2	23	16	AAV56766	Human bcr/abl b2-a
C	18	15.4	64.2	23	16	AAV56766	Human bcr/abl b2-a
C	19	15.4	64.2	23	16	AAV56766	Chromosomal trans
C	20	15.4	64.2	52	17	AAI2637	T7 promoter-acute
C	21	15.4	64.2	60	17	AAI29713	Chronic myeloid le
C	22	15.4	64.2	62	15	AAO66773	l6(1131 ribozyme s
C	23	15.2	63.3	61	22	AAK96535	Human neuroregulin g
C	24	15.2	63.3	61	22	AAK98028	Human neuroregulin g
C	25	15.2	62.5	33	17	AAI10495	BCR-ABL oncogene f
C	26	15.2	62.5	33	17	AAI10497	ABL oncogene Intro
C	27	15.2	62.5	34	21	AAZ24225	M. thermophila lac
C	28	15.2	62.5	47	15	AAO66785	Ribozyme substrate
C	29	15.2	62.5	60	24	ABN3928	Human spliced tran
C	30	15.2	62.5	65	24	ABN35678	Mouse spliced tran
C	31	15.2	62.5	80	14	AAQ34631	Human phi-positive
C	32	15.2	62.5	80	19	AAV20460	Human bcr-abl onco
C	33	14.8	61.7	31	20	AAV83517	Sense PCR primer 7
C	34	14.8	61.7	60	24	ABN38822	Forward PCR primer
C	35	14.6	60.8	38	21	AAZ61138	Human b2a2 sense p
C	36	14.4	60.0	23	14	AAQ34658	Human calcium sens
C	37	14.4	60.0	23	22	AAZ27985	Human b2a2 junctio
C	38	14.4	60.0	26	14	AAO34653	Human b2a2 junctio
C	39	14.4	60.0	26	15	AAO64687	Human b2a2 junctio
C	40	14.4	60.0	26	15	AAO57148	Chromosomal trans
C	41	14.4	60.0	26	15	AAO56493	Probe for 3SR ampl
C	42	14.4	60.0	26	19	AAV20478	Human b2/a2 bcr-ab
C	43	14.4	60.0	33	24	AAV01856	Oligodeoxynucleot
C	44	14.4	60.0	33	24	AAI72671	Human retinoblasto
C	45	14.4	60.0	59	19	AAV61667	Fusarium sp. 188 r

ALIGNMENTS

RESULT 1
AAZ60855 standard; DNA: 24 BP.
AAZ60855:
16-MAY-2000 (first entry)
Oligonucleotide used to detect bcr b3-abl fusion transcripts.
Fusion transcript; translocation; bcr b3 region; abl gene;
amplification assay; detection assay; medical diagnosis;
clinical monitoring; chimeric RNA; fusion RNA; condition marker;
disease marker; cancer; leukemia; ss.
Synthetic:
WO200005418-A1.
23-JUL-1999: 99WO-US16832.
23-JUL-1999: 99US-0121239.
(GENP-) GEN-PROBE INC.
Harvey RC, Eastman PS;
WPI: 2000-182730/16.
Novel methods for preparing RNA from biological samples, used for the

PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 XX
 PS Claim 19; Page 42; 49pp; English.
 CC
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;
 Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GTGGACATGAGCCCTTCAGCGG 24
 |||||||
 Db 1 GTGGACATGAGCCCTTCAGCGG 24
 RESULT 2
 AAZ60856
 ID AAZ60856 standard; RNA; 24 BP.
 AC
 AC AAZ60856;
 DT 16-MAY-2000 (first entry)
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 DE
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 OS Synthetic.
 OS
 PN WO200005418-A1.
 PD 03-FEB-2000.
 PF 23-JUL-1999; 99WO-US16832.
 PR 23-JUL-1998; 98US-0121239.
 PA (GENP-) GEN-PROBE INC.
 PI Harvey RC, Eastman PS;
 PI Harvey RC, Eastman PS;
 DR WPI; 2000-182730/16.
 XX
 XX Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 PS Claim 19; Page 42; 49pp; English.
 CC
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 U; 0 other;
 Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 83.3%; Pred. No. 0.088;
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GTGGACATGAGCCCTTCAGCGG 24
 |||||||
 Db 1 GTGGACATGAGCCCTTCAGCGG 24
 RESULT 3
 AAZ60857/c
 ID AAZ60857 standard; DNA; 24 BP.
 AC
 AC AAZ60857;
 DT 16-MAY-2000 (first entry)
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 DE
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 OS Synthetic.
 OS
 PN WO200005418-A1.
 PD 03-FEB-2000.
 PF 23-JUL-1999; 99WO-US16832.
 PR 23-JUL-1998; 98US-0121239.
 PA (GENP-) GEN-PROBE INC.
 PI Harvey RC, Eastman PS;
 PI Harvey RC, Eastman PS;
 DR WPI; 2000-182730/16.
 XX
 XX Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 PS Claim 19; Page 43; 49pp; English.
 CC
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

SO Sequence 24 BP: 4 A; 8 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGGACATGAGCCCTCAGCG 24
 ||||||||||||||||||||
 DB 24 GTGGACATGAGCCCTCAGCG 1

RESULT 4
 AA60858/C
 ID AA60858 standard; RNA; 24 BP.
 XX AA60858;
 AC
 XX
 DT 16-MAY-2000 (first entry)
 DE
 XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 XX
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO200005418-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 23-JUL-1999; 99WO-US16832.
 XX
 PR 23-JUL-1998; 98US-0121239.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Harvey RC, Eastman PS;
 XX
 DR WPI; 2000-182730/16.
 XX
 PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids -
 XX
 PS Claim 19; Page 43; 49pp; English.

CC Oligonucleotides AA60840-62 and AA60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

SO Sequence 24 BP: 4 A; 8 C; 6 G; 6 U; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGGACATGAGCCCTCAGCG 24
 ||||||||||||||||||||
 DB 24 GTGGACATGAGCCCTCAGCG 1

RESULT 5
 ABN38552
 ID ABN38552 standard; DNA; 60 BP.
 XX
 AC
 XX
 DT 15-JUL-2002 (first entry)
 DE
 XX Human spliced transcript detection oligonucleotide SEQ ID NO:11300.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 XX
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 PS Example 1; SEQ ID 11300; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN9589 represent

CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 60 BP; 16 A; 17 C; 17 G; 10 T; 0 other;

Query Match 71.7%; Score 17.2; DB 24; Length 60;
 Best Local Similarity 86.4%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GGACATGAGCCCTTCAGCG 24
 Db 23 GGACATGAGATCATCAGCTG 44

RESULT 6
 ABN54940
 ID ABN54940 standard; DNA; 65 BP.

AC ABN54940;

DE 15-JUL-2002 (first entry)

Mouse spliced transcript detection oligonucleotide SEQ ID NO:27688.

Human; mouse; rat; splice transcript; detection; RNA transcript;
 splice variant; transcriptome; oligonucleotide library; ss.

Mus musculus.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB01903.

28-JUL-2000; 2000US-221607P.

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which
 selectively hybridize to mRNAs transcribed from a transcription unit of
 a genome, useful for detecting tissue-, pathology-, and
 developmental-specific genes

Example 1; SEQ ID 27688; 47pp; English.

The present invention describes oligonucleotide libraries for detecting
 messenger RNAs that populate a (sub-)transcriptome, where the
 (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 transcription units that populate a genome. The library comprises
 several oligonucleotides, each capable of hybridizing selectively to a
 set of messenger RNAs transcribed from a given transcription unit of
 the genome, which encodes one or more messenger RNA splice variants.
 The oligonucleotide libraries are useful for detecting mRNAs from a
 biological sample, in expression profiling studies, in qualitatively or
 quantitatively characterizing the corresponding transcriptome, and in
 detecting RNA transcripts and splice variants of human or animal
 transcriptomes. The libraries may also be used as specialised mini
 libraries to detect transcripts of a sub-transcriptome under a
 particular biological or pathological state, and so allowing the
 detection of tissue- and pathology-specific genes such as those genes
 only expressed in specific tissue under a specific pathological
 condition; to detect developmental specific genes; and to detect RNA
 transcripts and splice variants of a transcriptome of a patient suffering
 from a particular disorder. ABN27253 to ABN59589 represent

CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 65 BP; 18 A; 16 C; 19 G; 12 T; 0 other;

Query Match 71.7%; Score 17.2; DB 24; Length 65;
 Best Local Similarity 86.4%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGACATGAGCCCTTCAGC 22
 Db 7 GTGACATGAGATCATCAGCTG 28

RESULT 7
 AAQ46947/c
 ID AAQ46947 standard; DNA; 56 BP.

AC AAQ46947;

DE 21-JAN-1994 (first entry)

Chronic myelogenous leukemia probe strand 2.

Chronic myelogenous leukemia; CMLa chimeric bcr/abl;

genetic translocation; target sequence; bcr/abl target sequence; ss.

Synthetic.

Key Location/Qualifiers
 misc_feature 1..30

FT /tag- a
 FT /note- "complementary to part of CMLa chimeric
 bcr/abl target sequence"

FT misc_feature 31..40
 FT /tag- b
 FT /note- "complementary to nucleotides 36-27 of
 probe strand 1 (AAQ46946)"

FT misc_feature 41..56
 FT /tag- c
 FT /note- "complementary to nucleotides 16,1 of
 probe strand 3 (AAQ46948)"

EP552931-A.

28-JUL-1993.

20-JAN-1993; 93EP-0300377.

22-JAN-1992; 92US-0827021.

(GERR-) GEN PROBE INC.

Arnold LJ, Bezerkov R, Hogan JT, Nelson NC;

WPI; 1993-236606/30.

Nucleic acid molecules which hybridise in presence of target
 nucleic acid - are used as probes in hybridisation assays or as
 therapeutic agents for diseases

Example 5; Fig 10; 58pp; English.

A probe for detection of a target sequence corresponding to the
 major genetic translocation associated with chronic myelogenous
 leukaemia consists of three separate strands (see AAQ46946-8).
 Strands 1 and 2 form a 3-way junction with the target and strand 3
 forms a 3-way junction with the other two. Hybridisation of strand
 3 is completely target-dependent even though it does not come into

RESULT 10
AADI6331/c
ID AADI6331 standard; DNA; 35 BP.
XX
AC AADI6331;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human KOD delta (removed) death domain mutant constructing primer #2.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
KW cytosolic; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6267956-B1.
XX
PD 31-JUL-2001.
XX
PF 21-MAR-2000; 2000US-0531914.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (ZENE) ZENECA LTD.
XX
PI Gomes EC, Kasof GM, Prosser JC;
XX
DR WPI; 2001-535022/59.
XX
PT New human protein activator protein, useful for treating dysfunctional
PT apoptosis conditions and in screening assays to identify agonists which
PT agonize or mimic biological and/or pharmacological activity -
XX
PS Example 13; Column 53; 31pp; English.
XX
XS The invention relates to human protein activator of apoptosis and
XS methods to identify compounds that modulate the biological and/or
XS pharmacological activity of the activator and hence regulate
XS apoptosis. The nucleic acid and amino acid sequences of the kinase
XS of death (KOD) are useful for identifying compounds that modulate
XS the biological and/or pharmacological activity of a native mediator
XS of apoptosis, for treating dysfunctional apoptosis conditions, in
XS screening assays to identify agonists which agonise or mimic
XS biological and/or pharmacological activity, induce production of or
XS prolong the biological half-life of the molecule in vivo or in vitro.
XS The present sequence is a PCR primer used to synthesise human KOD
XS delta (removed) death domain mutant.
SQ Sequence 35 BP; 3 A; 12 C; 12 G; 8 T; 0 other:
XX
Query Match 65.0%; Score 15.6; DB 22; Length 35;
Best Local Similarity 81.8%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 GGAACATGAAGCCCTTCAGCGG 24
DB 35 GGAACACCAAGTCTTAAGCGG 14
IIIIII III IIII IIIII
RESULT 11
AASI2048
ID AASI2048 standard; DNA; 42 BP.
XX
AC AASI2048;
XX
DT 07-NOV-2001 (first entry)
XX
DE Antisense oligonucleotide used in study of PIP1L expression in rat brain.
XX
KW N-methyl-D-aspartate receptor; NMDA-R; protein tyrosine phosphatase; PTP;
KW vasotropic; cerebroprotective; vulnerary; neuroprotective; nootropic;
KW

KW anticonvulsant; neuroleptic; analgesic; PIP1L; ischaemic stroke; ss;
KW head trauma; brain injury; Huntington's disease; motor neuron disease;
KW spinocerebellar degeneration; epilepsy; neuropathic pain; chronic pain;
KW tolerance; schizophrenia; Alzheimer's disease; dementia; drug addiction;
KW psychosis; ethanol sensitivity; antisense; probe; rat; brain;
XX in situ hybridisation.
XX
OS Rattus sp.
XX
PN W0200157240-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US03049.
XX
PR 01-FEB-2000; 2000US-0179453.
XX
PA (AGYT-) AGY THERAPEUTICS INC.
XX
PI Melcher T, Kask K;
XX
DR WPI; 2001-522355/57.
XX
PT Identifying N-methyl-D-aspartate receptor signalling activity modulator,
PT involves detecting ability of agent to modulate activity of protein
PT tyrosine phosphatase on NMDA-R substrate or binding of PTP to NMDA-R -
XX
PS Example 4; Page 27; 34pp; English.
XX
XS The method of the invention comprises identifying a modulator of
XS N-methyl-D-aspartate receptor (NMDA-R) signalling activity by detecting
XS the ability of an agent to modulate the phosphatase activity of a protein
XS tyrosine phosphatase (PTP) e.g. PTP1, on an NMDA-R substrate or to
XS modulate the binding of PTP to NMDA-R. This method is useful for treating
XS diseases which are mediated by abnormal NMDA-R signalling, by
XS administering a modulator of PTP1 activity, thus modulating the level
XS of tyrosine phosphorylation of NMDA-R. Treatable diseases include
XS ischaemic stroke; head trauma or brain injury; Huntington's disease,
XS spinocerebellar degeneration, motor neuron diseases, epilepsy,
XS neuropathic pain, chronic pain, tolerance, schizophrenia, Alzheimer's
XS disease, dementia, psychosis, drug addiction and ethanol sensitivity.
XS This sequence represents an antisense oligonucleotide used in situ
XS hybridisation studies carried out to examine PTP1L expression in rat
XS brain.
SQ Sequence 42 BP; 9 A; 19 C; 6 G; 8 T; 0 other:
XX
Query Match 65.0%; Score 15.6; DB 22; Length 42;
Best Local Similarity 81.8%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 GGAACATGAAGCCCTTCAGCGG 24
DB 10 GCACACGGAAGCCCTTCAGCTG 31
IIIIII IIIII IIIII IIIII
RESULT 12
ABA73324
ID ABA73324 standard; DNA; 95 BP.
XX
AC ABA73324;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #21629.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN W0200157277-A2.
XX
PD 09-AUG-2001.

```

XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver.
XX
XX Claim 4; SEQ ID NO 21629; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 95 BP; 27 A; 21 C; 31 G; 16 T; 0 other;
XX
XX Query Match 65.0%; Score 15.6; DB 22; Length 95;
XX Best Local Similarity 81.8%; Pred. No. 9.2e+02;
XX Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 GTGGACATGAGCCCTTCAGC 22
XX | |||| | |||| |||| |
XX Db 51 GGGGAGATTAAGCCCTTCATC 72
XX
XX RESULT 13
XX ID AAK21762 standard; DNA; 95 BP.
XX AC AAK21762;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 21753.
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX

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PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 21753; 650pp + Sequence listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 95 BP; 27 A; 21 C; 31 G; 16 T; 0 other;
XX
XX Query Match 65.0%; Score 15.6; DB 22; Length 95;
XX Best Local Similarity 81.8%; Pred. No. 9.2e+02;
XX Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 GTGGACATGAGCCCTTCAGC 22
XX | |||| | |||| |||| |
XX Db 51 GGGGAGATTAAGCCCTTCATC 72
XX
XX RESULT 14
XX ID AAK47927 standard; DNA; 95 BP.
XX AC AAK47927;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 22484.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 22484; 658pp + Sequence listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX

```


GenCore version 5.1.3
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OM nucleic acid - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 : Search time 61.7878 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-26

Perfect score: 18

Sequence: 1 GGAATCAGCAGCAGCAGC 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: N_GenSeq 101002.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
7: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
16: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
17: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAZ60865	Oligonucleotide us
2	14.8	82.2	50	AAZ34141	Human PRO83 hbr1
3	14.8	82.2	50	AAZ34141	Human PRO83 hbr1
4	13.8	76.7	25	AAZ35206	Corn shrunken 1 in
5	13.8	76.7	37	AAZ35206	Fas intron 1 5' pc
6	13.8	76.7	73	AAZ35206	Asbysa gossypii ge
7	13.8	76.7	98	AAZ35206	RNA aptamer #26 fo
8	13.4	74.4	20	AAZ04133	PCR primer used to
9	13.4	74.4	20	AAZ03618	PCR primer used to

10	13.4	74.4	50	AAZ78629	Human silent SNP c
11	13.2	73.3	18	AAZ5810	Human/mouse tpat D
12	13.2	73.3	36	AAZ08598	Anti-EGFP hamster
13	13.2	73.3	36	AAZ7862	Anti-green fluores
14	13.2	73.3	65	AAZ7862	Cloning site from
15	13.2	73.3	65	AAZ7862	Mouse spliced tran
16	13.2	73.3	84	AAZ7862	184, reporter olig
17	12.8	71.1	23	AAZ98678	Adaptor ATG-sense
18	12.8	71.1	23	AAZ98678	Ras target protein
19	12.8	71.1	45	AAZ98678	Human SNP oligonuc
20	12.8	71.1	50	AAZ98678	Human spliced tran
21	12.8	71.1	50	AAZ98678	EST clone DF909.
22	12.8	71.1	65	AAZ98678	Human nervous syst
23	12.8	71.1	80	AAZ98678	RNA aptamer #27 fo
24	12.8	71.1	90	AAZ98678	Human immune/haem
25	12.8	71.1	95	AAZ98678	Human immune/haem
26	12.8	71.1	95	AAZ98678	Human immune/haem
27	12.8	71.1	95	AAZ98678	Human immune/haem
28	12.8	71.1	95	AAZ98678	Human immune/haem
29	12.8	71.1	95	AAZ98678	Human immune/haem
30	12.8	71.1	95	AAZ98678	Human immune/haem
31	12.8	71.1	95	AAZ98678	Human immune/haem
32	12.8	71.1	100	AAZ98678	Human immune/haem
33	12.8	71.1	100	AAZ98678	Human immune/haem
34	12.4	68.9	20	AAZ98678	Human immune/haem
35	12.4	68.9	20	AAZ98678	Human immune/haem
36	12.4	68.9	24	AAZ98678	Human immune/haem
37	12.4	68.9	24	AAZ98678	Human immune/haem
38	12.4	68.9	24	AAZ98678	Human immune/haem
39	12.4	68.9	24	AAZ98678	Human immune/haem
40	12.2	67.8	23	AAZ98678	Human immune/haem
41	12.2	67.8	24	AAZ98678	Human immune/haem
42	12.2	67.8	24	AAZ98678	Human immune/haem
43	12.2	67.8	25	AAZ98678	Human immune/haem
44	12.2	67.8	27	AAZ98678	Human immune/haem
45	12.2	67.8	37	AAZ98678	Human immune/haem

ALIGNMENTS

RESULT 1
AAZ60865 standard; RNA; 18 BP.
AAZ60865:
16-MAY-2000 (first entry)
Oligonucleotide used to detect bcr b3-abl fusion transcripts.
Fusion transcript; translocation; bcr b3 region; abl gene;
amplification assay; detection assay; medical diagnosis;
clinical monitoring; chimeric RNA; fusion RNA; condition marker;
disease marker; cancer; leukemia; ss.
Synthetic.
WO200005416-A1.
03-FEB-2000.
23-JUL-1999; 99WO-0516832.
23-JUL-1998; 98US-0121339.
(GENP-) GEN-PROBE INC.
Harvey RC, Eastman PS;
WPI: 2000-182730/16.
Novel methods for preparing RNA from biological samples, used for the

PR detection and measurement of nucleic acids and fusion nucleic acids -
XX
PS Claim 19; Page 44; 49pp; English.
XX
CC Oligonucleotides AA60840-62 and AA60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.
XX
S0 Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATGG 18
Db 1 GGAATCATCGAGCATGG 18
|||||
ID AA234141 standard; DNA; 50 BP.
XX AA234141:
XX
AC 07-DEC-1999 (first entry)
XX
DT Human PRO983 hybridisation probe.
XX
DE
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Synthetic.
XX
SS Homo sapiens.
XX
PN WO946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.

PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081193.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081953.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083544.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083555.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084459.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086450.
PR 28-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 30-JUL-1998; 98US-0087208.
PR 11-SEP-1998; 98US-0100038.


```

XX (GETH ) GENENTECH INC.
PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Example 45; Page 220; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA23891 to
XX AA234338, and AA41685 to AA41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX
XX Sequence 50 BP; 13 A; 10 C; 13 G; 14 T; 0 other;
SQ
Query Match 82.2%; Score 14.8; DB 20; Length 50;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCGATCG 18
Db 5 GGAATCATCGAGCGAGG 22
|||||
RESULT 3
AAC78779 AAC78779 standard; DNA; 50 BP.
XX ID AAC78779;
XX AC AAC78779;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human PRO983 hybridisation probe SEQ ID NO:294.
XX
XX Human: secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX expressed sequence tag; detection; cancer; PCR primer; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200053756-A2.
XX
XX 14-SEP-2000.
XX
XX 18-FEB-2000; 2000WO-US04341.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0145698.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 16-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.

```

```

PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers J, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Kijavrin JJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2000-611443/58.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities -
XX
XX Example 45; Page 275; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytosolic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX
XX Sequence 50 BP; 13 A; 10 C; 13 G; 14 T; 0 other;
SQ
Query Match 82.2%; Score 14.8; DB 21; Length 50;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCGATCG 18
Db 5 GGAATCATCGAGCGAGG 22
|||||
RESULT 4
AAZ35206/C AAZ35206 standard; DNA; 25 BP.
XX ID AAZ35206;
XX AC AAZ35206;
XX
XX 13-MAR-2000 (first entry)
XX
XX Corn shrunken 1 intron 1/exon 1 PCR primer.
XX
XX Corn: maize; transgenic plant; lipid; food; feedstuff;
XX vegetable oil; seed oil; fatty acid desaturase; oleosin; promoter;
XX shrunken; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Zea mays.
XX
XX WO9964579-A2.
XX
XX 16-DEC-1999.
XX
XX 09-JUN-1999; 99WO-US12884.
XX
XX 11-JUN-1998; 98US-0088987.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Shen JB;
XX WPI; 2000-097535/08.

```

PT New maize oleosin promoter, used for producing transgenic plants with
 altered fatty acid composition of the oil, used e.g. in animal feeds
 XX
 PS Example 6; Page 38; 108bp; English.
 CC This primer was used in the PCR amplification of the corn shrunken
 CC gene intron/exon1 region. The PCR product was used in an
 CC expression cassette utilized in oleosin 16 kDa promoter deletion
 CC studies. The invention relates to the preparation and use of
 CC nucleic acid fragments comprising a corn oleosin promoter (see
 CC AA35165-77), a stearyl-ACP desaturase (see AA235179-80) and/or a
 CC delta-12 desaturase (see AA235178) nucleic acid, which can be used to
 CC modify the lipid profile, e.g. the stearic acid or oleic acid
 CC content, of corn. Transgenic corn plants, their seeds, and oil
 CC produced from them are also claimed.
 XX
 SQ Sequence 25 BP; 3 A; 7 C; 8 G; 7 T; 0 other;
 Query Match 76.7%; Score 13.8; DB 21; Length 25;
 Best Local Similarity 88.2%; Pred. No. 5.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 2 GAATCATCGAGCATGG 18
 DB 25 GAACCATCGAGCATGG 9
 RESULT 5
 AA093882
 ID AA093882 standard; cDNA; 37 BP.
 XX
 AC AA093882;
 XX
 DT 06-NOV-1995 (first entry)
 XX
 DE Fas intron 1 5' PCR primer.
 XX
 KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
 KW adoptive immunotherapy; transgenic animal; primer; PCR;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 FN W09513701-A.
 XX
 PD 26-MAY-1995.
 XX
 PF 15-NOV-1994; 94WO-US13173.
 XX
 PR 15-NOV-1993; 93US-0152443.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC, Shapiro JP;
 XX
 DR WPI; 1995-200120/26.
 XX
 PT New nucleic acid encoding Fas protein without its trans-membrane region
 PT - and related vectors, transformed cells, transgenic animals, protein and
 PT antibodies, useful for control of Fas mediated apoptosis
 XX
 PS Example 2; Page 14; 38bp; English.
 CC The intron-exon organization of the Fas transmembrane region was
 CC determined by PCR. Primers were designed to flank each of the
 CC putative introns, 1 and 2. The forward and reverse primers
 CC flanking intron 1 are given in AA093882-83, and those for intron 2
 CC in AA093884-85.
 XX
 SQ Sequence 37 BP; 12 A; 8 C; 8 G; 9 T; 0 other;
 Query Match 76.7%; Score 13.8; DB 16; Length 37;
 Best Local Similarity 88.2%; Pred. No. 5.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GAATCATCGAGCATG 17
 DB 14 GAATCATCAAGCAATG 30
 RESULT 6
 ABK16421
 ID ABK16421 standard; DNA; 73 BP.
 XX
 AC ABK16421;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Ashbya gossypii genomic DNA PCR primer #16.
 XX
 KW Fungal growth; fungicide; ss; PCR primer.
 XX
 OS Ashbya gossypii.
 OS Synthetic.
 XX
 PN US6307037-B1.
 XX
 PD 23-OCT-2001.
 XX
 PF 21-JUL-2000; 2000US-0625188.
 XX
 PR 21-JUL-2000; 2000US-0625188.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Gaffney TD, Flavier A, Cloyd Kirksey WM, Philippesen P, Dietrich F;
 PI Wendland J, Bernasconi P, White K, Filipowicz W;
 XX
 DR WPI; 2002-054476/07.
 XX
 PT New enzyme, useful as a fungicide to suppress the growth of pathogenic
 PT fungi, comprises IPC synthase, AURI gene (Me017), derived from Ashbya
 PT gossypii.
 XX
 PS Example 1; Column 20; 48bp; English.
 XX
 CC The invention relates to Ashbya gossypii polynucleotides which encode
 CC polypeptides essential for normal fungal growth and development. The
 CC sequences are useful for identifying inhibitors which can be used as
 CC fungicides to suppress the growth of pathogenic fungi. The proteins are
 CC useful in discovering new fungicides, based on the essentiality of the
 CC gene for normal growth and development. Sequences ABK16406-ABK16429
 CC represent PCR primers specific for the Ashbya gossypii polynucleotides,
 CC used in the methods of the invention.
 XX
 SQ Sequence 73 BP; 23 A; 16 C; 17 G; 17 T; 0 other;
 Query Match 76.7%; Score 13.8; DB 24; Length 73;
 Best Local Similarity 88.2%; Pred. No. 5.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GAATCATCGAGCATG 17
 DB 44 GATCATCGAGCATG 60
 RESULT 7
 AA299049
 ID AA299049 standard; RNA; 98 BP.
 XX
 AC AA299049;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE RNA aptamer #26 for binding Ras target protein.

KW Ras target protein; malignant tumour; signal transduction regulation;
 KW cell proliferation; cell differentiation; aptamer; inflammation; ss.
 OS Homo sapiens.
 XX WO200009684-A1.
 XX PD 24-FEB-2000.
 XX PF 13-AUG-1999; 99WO-JP04399.
 XX PR 14-AUG-1998; 98JP-0242596.
 XX PR 24-NOV-1998; 98JP-0333284.
 XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX PI Yokoyama S, Hirao I, Sakamoto K;
 XX DR WPI: 2000-224330/19.
 XX DR Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras
 PT target protein like Raf-1, useful in drug compositions to treat and
 PT diagnose malignant tumours and inflammation
 XX PS Claim 6; Page 41; 59pp; Japanese.
 XX CC The invention relates to novel nucleic acids which bind specifically
 CC to the target protein of Ras, e.g. Raf-1. RNA aptamer (AA299024-299051)
 CC based on these sequences are useful in the treatment and diagnosis of
 CC malignant tumours and inflammation. The nucleic acids can be used to
 CC formulate medicinal compositions that are useful in the treatment of
 CC malignant tumours and inflammation and for disease diagnosis by binding
 CC specifically to Ras target protein and regulating transmission of signal
 CC causing proliferation or differentiation of cells.
 XX SQ Sequence 98 BP; 24 A; 24 C; 26 G; 24 U; 0 other;
 OY Query Match 76.7%; Score 13.8; DB 21; Length 98;
 Best Local Similarity 70.6%; Pred. No. 6.1e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GGATCATCGAGGCATG 17
 11 GAATUCATCGAGGCATG 27
 ID AA204133 standard; DNA; 20 BP.
 XX AC AA204133;
 XX DT 07-OCT-1999 (first entry)
 XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritrititis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
 XX OS Synthetic.
 XX OS Chlamydia trachomatis.
 XX PN WO9928475-A2.
 XX PD 10-JUN-1999.
 XX PF 27-NOV-1998; 98WO-IB01939.
 XX PR 04-NOV-1998; 98US-0107077.
 XX PR 28-NOV-1997; 97ER-0015041.
 XX PR 17-DEC-1997; 97ER-0016034.

XX (GIST) GENSET.
 XX Griffais R;
 XX WPI: 1999-371125/31.
 XX PT Genome sequence of Chlamydia trachomatis
 XX PS Disclosure; Page 1663; 1755pp; English.
 XX CC PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
 CC encode polypeptides (see AA201425-206209) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 XX SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;
 OY Query Match 74.4%; Score 13.4; DB 20; Length 20;
 Best Local Similarity 93.3%; Pred. No. 8.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 GAATCATCGAGGCAT 16
 5 GAATCATCGAGGCAT 19
 ID AA203618/C
 XX AA203618 standard; DNA; 20 BP.
 XX AC AA203618;
 XX DT 07-OCT-1999 (first entry)
 XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritrititis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
 XX OS Synthetic.
 XX OS Chlamydia trachomatis.
 XX PN WO9928475-A2.
 XX PD 10-JUN-1999.
 XX PF 27-NOV-1998; 98WO-IB01939.
 XX PR 04-NOV-1998; 98US-0107077.
 XX PR 28-NOV-1997; 97ER-0015041.
 XX PR 17-DEC-1997; 97ER-0016034.
 XX PA (GIST) GENSET.
 XX PI Griffais R;
 XX DR WPI: 1999-371125/31.
 XX PT Genome sequence of Chlamydia trachomatis
 XX PS Disclosure; Page 1621; 1755pp; English.

CC PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC perihepatitis, Bartholinitis; pneumonia in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 XX

SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 other;

Query Match 74.4%; Score 13.4; DB 20; Length 20;
 Best Local Similarity 93.3%; Pred. No. 8.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAATCATCGAGGCAT 16
 |||||
 DB 16 GAATCATCGAGGCAT 2

RESULT 10

AA178629

ID AA178629 standard; DNA; 50 BP.

AC AA178629;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:5570.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KM Protein therapy; vaccine; probe; diagnostic assay; detection;

KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PE 30-NOV-2000; 2000WO-US2758.

PR 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -

PS Claim 1; Page 2214; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AA173060 to AA179867 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patient's own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids

CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.
 XX

SQ Sequence 50 BP; 13 A; 14 C; 13 G; 10 T; 0 other;

Query Match 74.4%; Score 13.4; DB 22; Length 50;
 Best Local Similarity 93.3%; Pred. No. 9.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATCATCGAGGCATCG 18
 |||||
 DB 17 ATCATCGAGGCATCG 31

RESULT 11

AAH25810/c

ID AAH25810 standard; DNA; 18 BP.

AC AAH25810;

DT 20-AUG-2001 (first entry)

DE Human/mouse Iba1 DNA PCR primer #1.

XX Human; mouse; immunomodulatory; monocyte; macrophage; inhibitor;

KM PCR primer; ss.

XX Unidentified.

PN JP2001078775-A.

PD 27-MAR-2001.

PE 14-SEP-1999; 99JP-0260793.

PR 14-SEP-1999; 99JP-0260793.

PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.

PA (MOCH) MOCHIDA PHARM CO LTD.

DR WPI; 2001-313369/33.

PT A macrophage function modifier useful for preventing and treating
 PT diseases caused by the increase or decrease in macrophage activity or
 PT function -

PS Example 2; Page 8; 20pp; Japanese.

CC The present invention provides a number of murine and human Iba1
 CC derivatives, which are capable of inhibiting the function of cells with
 CC monocyte or macrophage activity. These can be used as immunomodulators
 CC to prevent and treat diseases caused by a decrease or increase in the
 CC activity or the function of macrophages or an activator or an inhibitor
 CC of the function of cells of macrophage type. The present sequence is a
 CC PCR primer used in the exemplification of the invention.
 XX

SQ Sequence 18 BP; 4 A; 7 C; 2 G; 5 T; 0 other;

Query Match 73.3%; Score 13.2; DB 22; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGATCATCGAGGCATGG 18
 |||||
 DB 18 GGATCATCGAGGCATGG 1

RESULT 12

```

AAZ08588/c
ID AAZ08588 standard; DNA; 36 BP.
XX
XX AAZ08588;
AC
XX
XX 15-OCT-1999 (first entry)
DE
XX Anti-EgFP hammerhead ribozyme nucleotide sequence #20.
XX
XX Zinc finger motif; hammerhead ribozyme; combinatorial library;
KW apoptosis; cell cycle regulation; therapeutic; ss.
XX
XX Synthetic.
XX
XX WO941371-A1.
XX
XX 19-AUG-1999.
XX
XX 12-FEB-1999; 99WO-US03166.
XX
XX 13-FEB-1998; 98US-0023992.
XX
XX (STRA-) STRATA BIOSCIENCES INC.
XX
XX Keck JG, Wong JGP;
XX
XX WPI; 1999-494535/41.
XX
XX New combinatorial ribozyme library
XX
XX Disclosure; Fig 2; 66pp; English.
XX
XX The present invention describes a combinatorial ribozyme library (I)
XX comprising a double-stranded DNA with degenerate binding regions, a
XX means for determining directionality of expression, and a sense and
XX antisense strand, the sense strand coding for a catalytic domain, which
XX when expressed as RNA disrupts mRNA expression from a target nucleic
XX acid encoding a motif of interest. The combinatorial library (I) is
XX useful for assigning a function to a target nucleic acid encoding a
XX motif of interest. These nucleic acids may be involved in apoptosis or
XX cell cycle regulation, so are useful in therapeutics. (I) can be used
XX as a high throughput ribozyme based screening system that limits the
XX potential target sequences for evaluation to those which have an
XX increased probability of being associated with a molecular pathway that
XX is related to a disease or phenotype. This prevents cleavage of
XX housekeeping genes which will compromise cell function, as seen in the
XX prior art, and genes involved in functions are more likely to be
XX cleaved. More than one library can be introduced into host cells
XX simultaneously, allowing isolation of genes containing combinations of
XX motifs. The present sequence represents an anti-EgFP hammerhead ribozyme
XX nucleotide sequence which is used in the exemplification of the present
XX invention.
XX
XX Sequence 36 BP; 10 A; 8 C; 12 G; 6 T; 0 other:
SQ
Query Match 73.3%; Score 13.2; DB 20; Length 36;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAAATCATCGAGGCATGG 18
DB 18 GGACTCATCAGGCATGG 1
RESULT 13
AAZ78672/c
ID AAZ78672 standard; DNA; 36 BP.
XX
XX AAZ78672;
AC
XX
XX 03-SEP-1999 (first entry)
XX
XX Anti-green fluorescent protein ribozyme encoding oligonucleotide 20.

```

```

XX
XX Green fluorescent protein; GFP; anti-GFP; ribozyme; catalytic RNA;
KW antisense; target; directionality; high-throughput screen; cleavage;
XX gene function; virus replication; life cycle; antimicrobial; ds.
XX
XX Synthetic.
XX
XX WO9932618-A1.
XX
XX 01-JUL-1999.
XX
XX 18-DEC-1998; 98WO-US27942.
XX
XX 19-DEC-1997; 97US-0995234.
XX
XX (STRA-) STRATA BIOSCIENCES INC.
XX
XX Keck JG, Kuo SS, Molony JM;
XX
XX WPI; 1999-405170/34.
XX
XX Non-bacterial cloning in delivery and expression of nucleic acids
XX
XX Example 1; Fig 1C; 64pp; English.
XX
XX This invention describes a novel double-stranded DNA which encodes a
XX catalytic RNA targeted to an mRNA of a gene of interest and has a means
XX for determining directionality of expression. The double-stranded DNA
XX comprises a sense strand and an antisense strand. The sense strand codes
XX for an antisense strand, which when expressed as RNA binds to an mRNA
XX sequence transcribed from a target nucleic acid sequence, so that
XX expression of a product of the target nucleic acid sequence is inhibited. A means
XX for determining directionality of expression is included in the
XX double-stranded DNA. The methods and compositions are described in
XX high-throughput screens to assign gene functions of genes of interest.
XX Cleavage of the mRNA results in an altered phenotype from which the
XX function of a product encoded by the mRNA is determined. The function of
XX genes can be identified that are involved in bacteria or microorganism
XX cycle. If the targeted nucleic acid is in a bacteria or microorganism,
XX determining their function identifies new pathways and lead to the
XX identification of targets for new antimicrobials. The ability to
XX eliminate the amplification step of plasmid DNA in bacteria such as
XX Escherichia coli is a major cost saving step as well as a time saving
XX step over existing technologies. E. coli amplification can add several
XX days onto the entire process. The new method lends itself to automation
XX when implemented in a 96-well or similar multi-well format.
XX High-throughput delivery and expression of the molecules from a gene
XX vector family offers the advantage that multiple members of these
XX molecules can be introduced into and expressed in host cell cultures to
XX enable identification of genes by a manageable screening process.
XX Directionality is achieved by incorporation of unique restriction
XX sites at both ends of synthetic oligonucleotides used to prepare
XX double-stranded DNA. This sequence represents an oligonucleotide which
XX encodes an anti-green fluorescent protein (GFP) ribozyme.
XX
XX Sequence 36 BP; 10 A; 8 C; 12 G; 6 T; 0 other:
SQ
Query Match 73.3%; Score 13.2; DB 20; Length 36;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAAATCATCGAGGCATGG 18
DB 18 GGACTCATCAGGCATGG 1
RESULT 14
AAZ99099/c
ID AAZ99099 standard; DNA; 65 BP.
XX
XX AAZ99099;
AC
XX
XX 21-JUN-2000 (first entry)
XX

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XX DE Cloning site from plasmid pBAC-PAK-poly(His).
XX PI
XX KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ds;
XX KW two-hybrid screen; signal transduction.
XX OS Synthetic.
XX PN FR2782084-A1.
XX PD 11-FEB-2000.
XX PF 04-AUG-1998; 98FR-0009997.
XX PR 04-AUG-1998; 98FR-0009997.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Elbaz N, Nahmias C, Strosberg AD;
XX DR WPI: 2000-248410/22.
XX DR P-PSDB; AAY83783.
XX PT Nucleic acids coding for angiotensin II receptor AT2 interacting
XX PT proteins useful in screening assays for receptor-protein interaction
XX PS Example 3; Fig 8; 63pp; French.
XX CC This sequence represents the cloning site from the plasmid
XX CC pBAC-PAK-poly(His) used for expression of the "short" clone of the mouse
XX CC angiotensin II (AT2) receptor interacting protein (ATIP; AAY83777).
XX CC Cells transformed with vectors containing the cDNA, or immobilized
XX CC proteins encoded by it, can be used to screen for substances that
XX CC modulate ATIP-AT2 interaction or substances that interact with ATIP,
XX CC especially using yeast two- or three-hybrid techniques. Such substances
XX CC may be useful for treating disorders associated with anomalous AT2
XX CC receptor signal transduction.
XX SQ Sequence 65 BP; 12 A; 21 C; 18 G; 14 T; 0 other;
XX
XX Query Match 73.3%; Score 13.2; DB 21; Length 65;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCATGG 18
DB 45 GGAACACGAGCATGG 28

```

RESULT 15
ABN54496/C
ID ABN54496 standard; DNA; 65 BP.
XX AC ABN54496;
XX DT 15-JUL-2002 (first entry)
XX DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:27244.
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX KW splice variant; transcriptome; oligonucleotide library; ss.
XX OS Mus musculus.
XX PN WO200210449-A2.
XX PD 07-FEB-2002.
XX PF 20-JUL-2001; 2001WO-IB01903.
XX PR 28-JUL-2000; 2000US-221607P.
XX PR 02-MAY-2001; 2001US-287724P.
XX

```

PA (COMP-) COMPUGEN INC.
XX PI
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX DR WPI: 2002-257383/30.
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of
XX PT a genome, useful for detecting tissue-, pathology-, and
XX PT developmental-specific genes.
XX PS Example 1; SEQ ID 27244; 47pp; English.
XX
XX CC The present invention describes oligonucleotide libraries for detecting
XX CC messenger RNAs that populate a (sub-)transcriptome, where the
XX CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX CC transcription units that populate a genome. The library comprises
XX CC several oligonucleotides, each capable of hybridizing selectively to a
XX CC set of messenger RNAs transcribed from a given transcription unit of
XX CC the genome, which encodes one or more messenger RNA splice variants.
XX CC The oligonucleotide libraries are useful for detecting mRNAs from a
XX CC biological sample, in expression profiling studies, in qualitatively or
XX CC quantitatively characterizing the corresponding transcriptome, and in
XX CC detecting RNA transcripts and splice variants of human or animal
XX CC transcriptomes. The libraries may also be used as specialised mini
XX CC libraries to detect transcripts of a sub-transcriptome under a
XX CC particular biological or pathological state, and so allowing the
XX CC detection of tissue- and pathology-specific genes such as those genes
XX CC only expressed in specific tissue under a specific pathological
XX CC condition; to detect developmental specific genes; and to detect RNA
XX CC transcripts and splice variants of a transcriptome of a patient suffering
XX CC from a particular disorder. ABN27253 to ABN59589 represent
XX CC oligonucleotide sequences from rats, humans and mice, which are used in
XX CC the exemplification of the present invention.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.int/pub/published_pct_sequences.
XX SQ Sequence 65 BP; 20 A; 18 C; 12 G; 15 T; 0 other;
XX
XX Query Match 73.3%; Score 13.2; DB 24; Length 65;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCATGG 18
DB 19 GGGATCATCGAGCATGG 2

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Search completed: December 21, 2002, 11:54:46
Job time : 64.7878 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 ; Search time 89.249 Seconds
(without alignments)
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Title: US-09-121-239-27

Sequence: 1 CACTCAGCCACTGGATTTAAGCAGAG 26

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

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Maximum DB seq length: 100
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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20	/SIDS2/gcgadta/geneseq/genseqn-emb1/NA1999.DAT.*
21	/SIDS2/gcgadta/geneseq/genseqn-emb1/NA2000.DAT.*
22	/SIDS2/gcgadta/geneseq/genseqn-emb1/NA2001.DAT.*
23	/SIDS2/gcgadta/geneseq/genseqn-emb1/NA2002.DAT.*
24	/SIDS2/gcgadta/geneseq/genseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	100.0	26	21	AAZ69866	Oligonucleotide us
2	26	100.0	52	19	AAZ69188	Antisense RNA sequ
3	26	100.0	53	19	AAV01789	Antisense RNA sequ
4	26	100.0	54	19	AAV01790	Antisense RNA sequ
5	26	100.0	55	19	AAV01791	Antisense RNA sequ
6	26	100.0	56	14	AAQ46930	Branched probe to
7	26	100.0	56	19	AAV01782	Antisense RNA sequ
8	26	100.0	57	19	AAV01783	Antisense RNA sequ
9	26	100.0	58	19	AAV01794	Antisense RNA sequ

C	10	26	100.0	59	19	AAAV01795
C	11	125	96.2	40	21	AAAB69141
C	12	125	96.2	41	21	AAAB69135
C	13	125	96.2	59	10	AAAN97243
	14	25	96.2	59	10	AAAN97244
	15	25	96.2	59	15	AAOS56680
	16	25	96.2	59	15	AAOS56681
	17	25	96.2	59	20	AAZ092294
	18	25	96.2	59	20	AAZ092295
	19	25	96.2	59	21	AAZ602320
	20	25	96.2	59	21	AAZ602330
	21	25	96.2	60	17	AAT828714
	22	25	96.2	66	17	AAQ485946
	23	25	96.2	40	19	AAV35474
	24	20	76.9	47	24	AAI720001
	25	19.4	74.6	47	24	AAI720035
	26	19.4	76.9	91	24	AAI71998
	27	19	73.1	41	24	AAI71999
	28	18	69.2	41	24	AAI72002
	29	18	69.2	18	13	AAO21921
	30	18	69.2	18	19	AAV39476
	31	18	69.2	50	22	AAI33825
	32	17.2	66.2	41	22	AAH41253
	33	16.8	64.6	31	22	AAI30925
	34	16	61.5	30	22	AAF59009
	35	16	61.5	39	14	AAO37185
	36	16	61.5	50	22	AAH89705
	37	16	61.5	50	22	AAH89705
	38	16	61.5	88	20	AAAX57895
	39	16	61.5	88	20	AAAX57878
	40	15.8	60.8	21	21	AAAP93002
	41	15.8	59.2	60	24	AAH44004
	42	15.4	59.2	80	22	AAI24014
	43	15.2	59.5	62	20	AAI13390
	44	15	57.7	22	21	AAAB6516
	45					

PF detection and measurement of nucleic acids and fusion nucleic acids -
 XX
 PS Claim 19; Page 44; 49pp; English.
 XX
 CC Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of RNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

SQ Sequence 26 BP; 8 A; 7 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGATTTAAGCAGAG 26
 ID AAV01788/c
 DB 1 CACTCAGCCACTGATTTAAGCAGAG 26

AAV01788/c
 ID AAV01788 standard; RNA; 52 BP.

AAV01788;
 04-JUN-1998 (first entry)
 Antisense RNA sequence of the specification.

Antisense; inhibitor; gene expression; chromosomal translocation;
 Translocation point; pharmaceutical composition;
 chronic myelogenous leukemia; acute lymphoblastic leukemia;
 acute myelogenous leukemia; Non-Hodgkin Lymphoma; treatment; ss.

Synthetic.

WO9746672-A2.

11-DEC-1997.

05-JUN-1997; 97WO-EP02923.

05-JUN-1996; 96EP-0109034.

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Haas R, Kronenwett R, Sczakiel G;

WPI: 1998-042181/04.

Nucleic acid molecule containing chromosomal translocation point -
 useful to treat chromosomal translocation disorders, e.g. chronic
 myelogenous leukemia

Claim 6; Page 37; 49pp; English.

AAV01779-804 represent antisense RNA sequences. For long chain antisense

CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary
 CC to a first and second chromosomal DNA sequence. The nucleic acid
 CC molecule forms at least part of a chromosomal translocation resulting in
 CC a fusion gene containing the translocation point. The DNA sequence, as
 CC well as vectors and host cells containing it are useful in
 CC pharmaceutical compositions for treating disorders based on chromosomal
 CC translocations, preferably for chronic myelogenous leukemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukemias, acute myelogenous leukemias and Non-Hodgkin Lymphomas.

SQ Sequence 52 BP; 12 A; 10 C; 16 G; 14 U; 0 other;

Query Match 100.0%; Score 26; DB 19; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGATTTAAGCAGAG 26
 ID AAV01789/c
 DB 43 CACTCAGCCACTGATTTAAGCAGAG 18

AAV01789/c
 ID AAV01789 standard; RNA; 53 BP.

AAV01789;
 04-JUN-1998 (first entry)
 Antisense RNA sequence of the specification.

Antisense; inhibitor; gene expression; chromosomal translocation;
 Translocation point; pharmaceutical composition;
 chronic myelogenous leukemia; acute lymphoblastic leukemia;
 acute myelogenous leukemia; Non-Hodgkin Lymphoma; treatment; ss.

Synthetic.

WO9746672-A2.

11-DEC-1997.

05-JUN-1997; 97WO-EP02923.

05-JUN-1996; 96EP-0109034.

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Haas R, Kronenwett R, Sczakiel G;

WPI: 1998-042181/04.

Nucleic acid molecule containing chromosomal translocation point -
 useful to treat chromosomal translocation disorders, e.g. chronic
 myelogenous leukemia

Claim 6; Page 37; 49pp; English.

AAV01779-804 represent antisense RNA sequences. For long chain antisense

RNA, the association rate with their target RNA in vitro correlates

with their effectiveness in vivo. Antisense molecules are potent

inhibitors of gene expression and viral functions. The antisense

molecules AAV01779-804 exemplify novel nucleic acid molecules of the

invention. These nucleic acid molecules contain portions complementary

to a first and second chromosomal DNA sequence. The nucleic acid

molecule forms at least part of a chromosomal translocation resulting in

a fusion gene containing the translocation point. The DNA sequence, as

well as vectors and host cells containing it are useful in

pharmaceutical compositions for treating disorders based on chromosomal

CC translocations, preferably for chronic myelogenous leukaemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 XX
 SO Sequence 53 BP; 13 A; 10 C; 16 G; 14 U; 0 other;
 Query Match 100.0%; Score 26; DB 19; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CACTCAGCCACTGGATTAAACGAG 26
 DB 43 CACTCAGCCACTGGATTAAACGAG 18
 RESULT 4
 AAV01790/c
 ID AAV01790 standard; RNA; 54 BP.
 AC AAV01790;
 XX
 XX 04-JUN-1998 (first entry)
 DT
 DE Antisense RNA sequence of the specification.
 XX
 XX Antisense; inhibitor; gene expression; chromosomal translocation;
 KW translocation point; pharmaceutical composition;
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
 XX
 XX Synthetic.
 OS
 XX W09746672-A2.
 PN
 XX 11-DEC-1997.
 PD
 XX 05-JUN-1997; 97WO-EP02923.
 PF
 XX 05-JUN-1996; 96EP-0109034.
 PR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Haas R, Kronenwett R, Szczakiel G;
 PI
 XX WPI; 1998-042181/04.
 DR
 XX Nucleic acid molecule containing chromosomal translocation point -
 PT useful to treat chromosomal translocation disorders, e.g. chronic
 PT myelogenous leukaemia
 PS
 XX Claim 6; Page 37; 49pp; English.
 CC AAV01779-804 represent antisense RNA sequences. For long chain antisense
 CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary
 CC to a first and second chromosomal DNA sequence. The nucleic acid
 CC molecule forms at least part of a chromosomal translocation resulting in
 CC a fusion gene containing the translocation point. The DNA sequence, as
 CC well as vectors and host cells containing it are useful in
 CC pharmaceutical compositions for treating disorders based on chromosomal
 CC translocations, preferably for chronic myelogenous leukaemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 CC
 SO Sequence 54 BP; 13 A; 10 C; 16 G; 15 U; 0 other;
 Query Match 100.0%; Score 26; DB 19; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAACGAG 26
 DB 43 CACTCAGCCACTGGATTAAACGAG 18
 RESULT 5
 AAV01791/c
 ID AAV01791 standard; RNA; 55 BP.
 AC AAV01791;
 XX
 XX 04-JUN-1998 (first entry)
 DT
 DE Antisense RNA sequence of the specification.
 XX
 XX Antisense; inhibitor; gene expression; chromosomal translocation;
 KW translocation point; pharmaceutical composition;
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
 XX
 XX Synthetic.
 OS
 XX W09746672-A2.
 PN
 XX 11-DEC-1997.
 PD
 XX 05-JUN-1997; 97WO-EP02923.
 PF
 XX 05-JUN-1996; 96EP-0109034.
 PR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Haas R, Kronenwett R, Szczakiel G;
 PI
 XX WPI; 1998-042181/04.
 DR
 XX Nucleic acid molecule containing chromosomal translocation point -
 PT useful to treat chromosomal translocation disorders, e.g. chronic
 PT myelogenous leukaemia
 PS
 XX Claim 6; Page 37; 49pp; English.
 CC AAV01779-804 represent antisense RNA sequences. For long chain antisense
 CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary
 CC to a first and second chromosomal DNA sequence. The nucleic acid
 CC molecule forms at least part of a chromosomal translocation resulting in
 CC a fusion gene containing the translocation point. The DNA sequence, as
 CC well as vectors and host cells containing it are useful in
 CC pharmaceutical compositions for treating disorders based on chromosomal
 CC translocations, preferably for chronic myelogenous leukaemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 CC
 SO Sequence 55 BP; 13 A; 10 C; 16 G; 16 U; 0 other;
 Query Match 100.0%; Score 26; DB 19; Length 55;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CACTCAGCCACTGGATTAAACGAG 26
 DB 43 CACTCAGCCACTGGATTAAACGAG 18
 RESULT 6
 AAQ46950
 ID AAQ46950 standard; DNA; 56 BP.
 AC AAQ46950;

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XX 21-JAN-1994 (first entry)
DE Branched probe to CM1A translocation region of chromosome 22.
XX
XX Chronic myelogenous leukaemia; CM1A chimeric bcr/abl;
XX acute lymphocytic leukaemia; ALL; genetic translocation;
XX chromosome 22; target sequence; universal detection oligomer;
XX branched probe; chemiluminescent acridinium ester; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..40
XX /tag= a
XX /note= "complementary to region of chromosome 22
XX associated with CM1A translocation"
XX
XX misc_feature 41..56
XX /tag= b
XX /note= "complementary to nucleotides 16-1 of
XX universal detection probe AAQ46949"
XX
XX EP552931-A.
XX
XX 28-JUL-1993.
XX
XX 20-JAN-1993; 93EP-0300377.
XX
XX 22-JAN-1992; 92US-0827021.
XX
XX (GEP- ) GEN PROBE INC.
XX
XX Arnold LJ, Bezverkov R, Hogan JJ, Nelson NC;
XX WPI; 1993-236606/30.
XX
XX Nucleic acid molecules which hybridise in presence of target
XX nucleic acid - are used as probes in hybridisation assays or as
XX therapeutic agents for diseases
XX
XX Example 6; Fig 12A; 58pp; English.
XX
XX Chimeric targets were synthesised homologous to 3 different
XX genetic translocations between a constant abl region of chromosome
XX 9 and various regions of chromosome 22; two are the most common
XX translocations associated with chronic myelogenous leukaemia (CM1A
XX and CM1b) and the other is associated with acute lymphocytic
XX leukaemia (ALL). An AE-labelled universal detection oligomer (AAQ46949)
XX specific for the abl region was synthesised. Three different
XX strands were designed to contain a probe region specific for one of
XX the translocated chromosome 22 regions as well as an arm region
XX complementary to part of the universal probe (AAQ46950-2). The probe
XX mixes were found to detect only the correct chimeric targets and
XX did not cross-react significantly with the other targets.
XX
XX Sequence 56 BP; 16 A; 17 C; 9 G; 14 T; 0 other;
SQ
Query Match 100.0%; Score 26; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CACTCAGCCACTGATTTAAGCAGAG 26
DB 10 CACTCAGCCACTGATTTAAGCAGAG 35

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XX Antisense RNA sequence of the specification.
DE
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin Lymphoma; treatment; ss.
XX
XX Synthetic.
XX
XX WO9746672-A2.
XX
XX 11-DEC-1997.
XX
XX 05-JUN-1997; 97WO-EP02923.
XX
XX 05-JUN-1996; 96EP-0109034.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSGEZENTRUM.
XX
XX Haas R, Kronenwett R, Sczakiel G;
XX WPI; 1998-042181/04.
XX
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX Claim 6; Page 37; 49pp; English.
XX
XX AA01779-804 represent antisense RNA sequences. For long chain antisense
XX RNA, the association rate with their target RNA in vitro correlates
XX with their effectiveness in vivo. Antisense molecules are potent
XX inhibitors of gene expression and viral functions. The antisense
XX molecules AA01779-804 exemplify novel nucleic acid molecules of the
XX invention. These nucleic acid molecules contain portions complementary
XX to a first and second chromosomal DNA sequence. The nucleic acid
XX molecule forms at least part of a chromosomal translocation resulting in
XX a fusion gene containing the translocation point. The DNA sequence, as
XX well as vectors and host cells containing it are useful in
XX pharmaceutical compositions for treating disorders based on chromosomal
XX translocations, preferably for chronic myelogenous leukaemia. The
XX pharmaceutical composition may also be used to treat acute lymphoblastic
XX leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
XX Sequence 56 BP; 13 A; 11 C; 16 G; 16 U; 0 other;
SQ
Query Match 100.0%; Score 26; DB 19; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CACTCAGCCACTGATTTAAGCAGAG 26
DB 43 CACTCAGCCACTGATTTAAGCAGAG 18

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RESULT 7
AAV01792/c
ID AAV01792 standard; RNA; 56 BP.
XX
XX AAV01792;
XX
XX 04-JUN-1998 (first entry)
DT

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RESULT 8
AAV01793/c
ID AAV01793 standard; RNA; 57 BP.
XX
XX AAV01793;
XX
XX 04-JUN-1998 (first entry)
DE
XX Antisense RNA sequence of the specification.
XX
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin Lymphoma; treatment; ss.
XX
XX Synthetic.
XX

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PN WO9746672-A2.
XX 11-DEC-1997.
PD 05-JUN-1997; 97WO-EP02923.
XX 05-JUN-1996; 96EP-0109034.
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Haas R, Kronenwett R, Szczakiel G;
XX WPI; 1998-042181/04.
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX Claim 6; Page 37; 49pp; English.
XX AAV01779-804 represent antisense RNA sequences. For long chain antisense
XX RNA, the association rate with their target RNA in vitro correlates
XX with their effectiveness in vivo. Antisense molecules are potent
XX inhibitors of gene expression and viral functions. The antisense
XX molecules AAV01779-804 exemplify novel nucleic acid molecules of the
XX invention. These nucleic acid molecules contain portions complementary
XX to a first and second chromosomal DNA sequence. The nucleic acid
XX molecule forms at least part of a chromosomal translocation resulting in
XX a fusion gene containing the translocation point. The DNA sequence, as
XX well as vectors and host cells containing it are useful in
XX pharmaceutical compositions for treating disorders based on chromosomal
XX translocations, preferably for chronic myelogenous leukaemia. The
XX pharmaceutical composition may also be used to treat acute lymphoblastic
XX leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
SQ Sequence 57 BP; 14 A; 11 C; 16 G; 16 U; 0 other;
Query Match 100.0%; Score 26; DB 19; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0; Gaps 0;
OY 1 CACTCAGCCACTGATTTAGCAGAG 26
DB 43 CACTCAGCCACTGATTTAGCAGAG 18
RESULT 9
AAV01794/C
ID AAV01794 standard; RNA; 58 BP.
XX AAV01794;
XX
XX 04-JUN-1998 (first entry)
XX
XX Antisense RNA sequence of the specification.
XX
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
XX
XX Synthetic:
XX MO9746672-A2.
XX 11-DEC-1997.
XX 05-JUN-1997; 97WO-EP02923.
XX 05-JUN-1996; 96EP-0109034.
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX

PI Haas R, Kronenwett R, Szczakiel G;
XX WPI; 1998-042181/04.
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX Claim 6; Page 37; 49pp; English.
XX AAV01779-804 represent antisense RNA sequences. For long chain antisense
XX RNA, the association rate with their target RNA in vitro correlates
XX with their effectiveness in vivo. Antisense molecules are potent
XX inhibitors of gene expression and viral functions. The antisense
XX molecules AAV01779-804 exemplify novel nucleic acid molecules of the
XX invention. These nucleic acid molecules contain portions complementary
XX to a first and second chromosomal DNA sequence. The nucleic acid
XX molecule forms at least part of a chromosomal translocation resulting in
XX a fusion gene containing the translocation point. The DNA sequence, as
XX well as vectors and host cells containing it are useful in
XX pharmaceutical compositions for treating disorders based on chromosomal
XX translocations, preferably for chronic myelogenous leukaemia. The
XX pharmaceutical composition may also be used to treat acute lymphoblastic
XX leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
SQ Sequence 58 BP; 14 A; 11 C; 17 G; 16 U; 0 other;
Query Match 100.0%; Score 26; DB 19; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0; Gaps 0;
OY 1 CACTCAGCCACTGATTTAGCAGAG 26
DB 43 CACTCAGCCACTGATTTAGCAGAG 18
RESULT 10
AAV01795/C
ID AAV01795 standard; RNA; 59 BP.
XX AAV01795;
XX
XX 04-JUN-1998 (first entry)
XX
XX Antisense RNA sequence of the specification.
XX
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
XX
XX Synthetic:
XX MO9746672-A2.
XX 11-DEC-1997.
XX 05-JUN-1997; 97WO-EP02923.
XX 05-JUN-1996; 96EP-0109034.
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Haas R, Kronenwett R, Szczakiel G;
XX WPI; 1998-042181/04.
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX Claim 6; Page 37; 49pp; English.
XX

CC AAV01779-804 represent antisense RNA sequences. For long chain antisense
CC RNA, the association rate with their target RNA in vitro correlates
CC with their effectiveness in vivo. Antisense molecules are potent
CC inhibitors of gene expression and viral functions. The antisense
CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
CC invention. These nucleic acid molecules contain portions complementary
CC to a first and second chromosomal DNA sequence. The nucleic acid
CC molecule forms at least part of a chromosomal translocation resulting in
CC a fusion gene containing the translocation point. The DNA sequence, as
CC well as vectors and host cells containing it are useful in
CC pharmaceutical compositions for treating disorders based on chromosomal
CC translocations, preferably for chronic myelogenous leukaemia. The
CC pharmaceutical composition may also be used to treat acute lymphoblastic
CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
SQ Sequence 59 BP; 15 A; 11 C; 17 G; 16 U; 0 other;
Query Match 100.0%; Score 26; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0; Gaps 0;
OY 1 CACTCAGCCACTGATTTAAGCAGAG 26
Db 43 CACTCAGCCACTGATTTAAGCAGAG 18
|||||
RESULT 11
ID AAA86914/C
AAA86914 standard; DNA; 40 BP.
XX
AC AAA86914;
XX
DT 15-JAN-2001 (first entry)
XX
DE Native bcr.
XX
KW Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;
KW single nucleotide polymorphism; identification; viral load; probe;
KW genotyping; medical marker diagnostic; primer; target; mutation;
KW genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO200049180-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-US04242.
XX
PR 18-FEB-1999; 99US-0252436.
PR 21-JUL-1999; 99US-0358972.
PR 25-AUG-1999; 99US-0383316.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;
PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;
XX
DR WPI; 2000-565377/52.
XX
PT Determining presence or absence of a predetermined endogenous nucleic
PT acid sequence by using an enzyme that depolymerizes the 3' end of an
PT oligonucleotide probe hybridized to a target sequence to release
PT identifier nucleotides -
XX
PS Example; Page 328; 389pp; English.
XX
CC The present invention describes a method (M1) for determining the
CC presence or absence of a predetermined endogenous nucleic acid target
CC sequence (ENAT). The method comprises hybridising a probe having an
CC identifier nucleotide (IN) with ENAT which is treated with an enzyme
CC that depolymerises the 3' end of hybridised NA to release the INs.
CC MI is used for determining the number of known sequence repeats present

CC in a nucleic acid target sequence in a nucleic acid sample. The method
CC is also useful for determining whether a nucleic acid target sequence in
CC a sample is an allele from a homozygous or heterozygous locus. The
CC method is also useful for detection of mutations, translocations and
CC SNPs in nucleic acids (including those associated with genetic disease),
CC determination of viral load, species identification, sample
CC contamination, and analysis of forensic samples. AAA86791 to AAA8709
CC and AAB12817 represent sequence which are used in the exemplification of
CC the present invention.
CC N.B. There is a discrepancy between the SEQ ID NO: and sequences given
CC in the examples, and the SEQ ID NO: and sequences given in the sequence
CC listing from the present invention.
XX
SQ Sequence 40 BP; 10 A; 9 C; 8 G; 13 T; 0 other;
Query Match 96.2%; Score 25; DB 21; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 ACTCAGCCACTGATTTAAGCAGAG 26
Db 40 ACTCAGCCACTGATTTAAGCAGAG 16
|||||
RESULT 12
ID AAA86915/C
AAA86915 standard; DNA; 41 BP.
XX
AC AAA86915;
XX
DT 15-JAN-2001 (first entry)
XX
DE bcr/abl translocation.
XX
KW Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;
KW single nucleotide polymorphism; identification; viral load; probe;
KW genotyping; medical marker diagnostic; primer; target; mutation;
KW genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO200049180-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-US04242.
XX
PR 18-FEB-1999; 99US-0252436.
PR 21-JUL-1999; 99US-0358972.
PR 25-AUG-1999; 99US-0383316.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;
PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;
XX
DR WPI; 2000-565377/52.
XX
PT Determining presence or absence of a predetermined endogenous nucleic
PT acid sequence by using an enzyme that depolymerizes the 3' end of an
PT oligonucleotide probe hybridized to a target sequence to release
PT identifier nucleotides -
XX
PS Example; Page 329; 389pp; English.
XX
CC The present invention describes a method (M1) for determining the
CC presence or absence of a predetermined endogenous nucleic acid target
CC sequence (ENAT). The method comprises hybridising a probe having an
CC identifier nucleotide (IN) with ENAT which is treated with an enzyme
CC that depolymerises the 3' end of hybridised NA to release the INs.
CC MI is used for determining the number of known sequence repeats present
CC in a nucleic acid target sequence in a nucleic acid sample. The method
CC is also useful for determining whether a nucleic acid target sequence in

CC a sample is an allele from a homozygous or heterozygous locus. The
 CC method is also useful for detection of mutations, translocations and
 CC SNPs in nucleic acids (including those associated with genetic disease),
 CC determination of viral load, species identification, sample
 CC contamination, and analysis of forensic samples. AA86791 to AA87079
 CC and AAB12817 represent sequence which are used in the exemplification of
 CC the present invention.
 CC N.B. There is a discrepancy between the SEQ ID NO: and sequences given
 CC in the examples, and the SEQ ID NO: and sequences given in the sequence
 CC listing from the present invention.
 XX
 SQ Sequence 41 BP; 9 A; 8 C; 11 G; 13 T; 0 other;
 Query Match 96.2%; Score 25; DB 21; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.029; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ACTCAGCCACTGGATTAAAGCAGAG 26
 DB 41 ACTCAGCCACTGGATTAAAGCAGAG 17
 RESULT 13
 AAN97243
 ID AAN97243-standard; DNA; 59 BP.
 AC AAN97243;
 XX 06-JUL-1993 (first entry)
 DT
 XX BCR/ABL target sequence.
 DE
 XX Deoxyoligonucleotide; probe; amine; label; acridinium ester; AE;
 KW hybridisation assay; protection; hydrolysis; stability;
 KW chimeric target sequence; chronic myelogenous leukemia; CML;
 KW translocation; abl; bcr; chromosome; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc-feature 31..59
 FT /*tag= a
 FT /label= abl-sequence
 W08902476-A.
 XX
 PD 23-MAR-1989.
 XX
 PE 21-SEP-1988; 88WO-US03195.
 XX
 PR 21-SEP-1987; 87US-0099392.
 XX
 PA (GEPH-) GEN PROBE INC.
 PA (MLTE-) ML TECHN VENTURES.
 XX
 PI Arnold LJ, Nelson NC, Arnold L;
 FI
 PL
 DR WPI; 1989-100016/13.
 XX
 XX Homogeneous binding assay using degradable label esp. acridinium
 XX ester - with different stabilities in bound and unbound forms,
 XX esp. useful in hybridisation detection of specific polynucleotide
 XX
 PS Example 16; Page 43; 64pp; English.
 XX
 CC Example 16 illustrates the detection of a chimeric target sequence
 CC associated with chronic myelogenous leukemia (CML) using a probe
 CC internally labelled with acridinium ester (AE).
 CC The probe (AAN97243) is complementary to the chimeric mRNA transcript
 CC (common break) associated with CML. This chimeric mRNA is a product
 CC of the chimeric gene formed by the translocation of a region of the
 CC abl gene on chromosome 9 into a region of chromosome 22 contg. the
 CC bcr gene. The BCR/ABL and ABL target sequences are given in



CC AAN97243-44. The AE-labelled probe was able to discriminate between
 CC chimeric target and normal sequences (as well as unhybridised probe) using
 CC the homogeneous binding assay.
 XX
 SQ Sequence 59 BP; 16 A; 17 C; 13 G; 13 T; 0 other;
 Query Match 96.2%; Score 25; DB 10; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ACTCAGCCACTGGATTAAAGCAGAG 26
 DB 1 ACTCAGCCACTGGATTAAAGCAGAG 25
 RESULT 14
 AAN97244
 ID AAN97244 standard; DNA; 59 BP.
 AC AAN97244;
 XX 06-JUL-1993 (first entry)
 DT
 XX ABL target sequence.
 DE
 XX Deoxyoligonucleotide; probe; amine; label; acridinium ester; AE;
 KW hybridisation assay; protection; hydrolysis; stability;
 KW chimeric target sequence; chronic myelogenous leukemia; CML;
 KW translocation; abl; bcr; chromosome; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc-feature 1..59
 FT /*tag= a
 FT /label= abl-sequence
 W08902476-A.
 XX
 PD 23-MAR-1989.
 XX
 PE 21-SEP-1988; 88WO-US03195.
 XX
 PR 21-SEP-1987; 87US-0099392.
 XX
 PA (GEPH-) GEN PROBE INC.
 PA (MLTE-) ML TECHN VENTURES.
 XX
 PI Arnold LJ, Nelson NC, Arnold L;
 FI
 PL
 DR WPI; 1989-100016/13.
 XX
 XX Homogeneous binding assay using degradable label esp. acridinium
 XX ester - with different stabilities in bound and unbound forms,
 XX esp. useful in hybridisation detection of specific polynucleotide
 XX
 PS Example 16; Page 43; 64pp; English.
 XX
 CC Example 16 illustrates the detection of a chimeric target sequence
 CC associated with chronic myelogenous leukemia (CML) using a probe
 CC internally labelled with acridinium ester (AE).
 CC The probe (AAN97243) is complementary to the chimeric mRNA transcript
 CC (common break) associated with CML. This chimeric mRNA is a product
 CC of the chimeric gene formed by the translocation of a region of the
 CC abl gene on chromosome 9 into a region of chromosome 22 contg. the
 CC bcr gene. The BCR/ABL and ABL target sequences are given in
 CC AAN97243-44. The AE-labelled probe was able to discriminate between
 CC chimeric target and normal sequences (as well as unhybridised probe) using
 CC the homogeneous binding assay.
 XX
 SQ Sequence 59 BP; 14 A; 15 C; 14 G; 16 T; 0 other;
 Query Match 96.2%; Score 25; DB 10; Length 59;

Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: December 21, 2002, 11:54:48
Job time : 91.249 secs

OY 2 ACTCAGCCACTGATTTAAGCAGAG 26
|||||
Db 1 ACTCAGCCACTGATTTAAGCAGAG 25

RESULT 15

AA055680
ID AA055680 standard; DNA; 59 BP.

AC AA055680;

DT 09-AUG-1994 (first entry)

DE N. gonorrhoeae 16S subunit BCR/ABL synthetic target sequence.

KW Probe; amine; linker arm; N-acridinium; ester; label; homogeneous;
hybridisation assay; detection; linear dilution series; Chlamydia;
rRNA; ss.

OS Synthetic.

PN US5283174-A.

PD 01-FEB-1994.

PF 21-SEP-1987; 87US-0099392.

PR 21-SEP-1987; 87US-0099392.

PR 12-DEC-1988; 88US-0294700.

PR 23-MAY-1990; 90US-0528920.

PR 08-NOV-1990; 90US-0613603.

PA (GENP-) GEN-PROBE INC.

PI Arnold LJ, Nelson NC;

DR WPI; 1994-048084/06.

PT Homogeneous nucleic acid hybridisation assay - using probe
labelled with acridinium ester for detection of linear dilution
series

PS Example 15; Column 25; 20pp; English.

CC The sequences given in AA055679-81 represent a probe, and a synthetic
and wild type target sequence which was used in the method of the
invention. The probes corresponds to the 16S subunit of *Neisseria*
gonorrhoeae and contains an amine linker arm which may bear an N-
acridinium ester label. Probes such as this may be used in an
homogeneous hybridisation assay for determining the presence or
amount of a target nucleic acid in a sample. This method comprises
contacting the sample with an N-acridinium bearing probe, such that
the acridinium ester label may be degraded by a chemical, eg. acid,
base or oxidising agent, while duplex-linked N-acridinium ester remains
undegraded. The hybridisation mixture is treated with the chemical and
the amount of undegraded N-acridinium ester is measured without
physically separating any unhybridised probe. The method is capable of
detecting linear dilution series, eg. *Chlamydia* rRNA with a detection
limit of 0.1-1 ng.

CC Sequence 59 BP; 16 A; 17 C; 13 G; 13 T; 0 other;

Query Match 96.2%; Score 25; DB 15; Length 59;

Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACTCAGCCACTGATTTAAGCAGAG 26
|||||
Db 1 ACTCAGCCACTGATTTAAGCAGAG 25

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 ; Search time 46.5061 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-1

Perfect score: 54
Sequence: 1 TAAATTATACGACTGCTCACTA.....CCCTGAGGCTCAAGTCAGA 54

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCITUS.COMB.seq.*
6: /cgn2_6/prodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	59.3	52	4	US-09-493-491-39 Sequence 39, Appl
2	32	59.3	54	4	US-09-493-491-29 Sequence 29, Appl
3	31	57.4	49	1	US-07-931-473B-50 Sequence 50, Appl
4	31	57.4	49	1	US-07-714-113C-50 Sequence 50, Appl
5	31	57.4	49	1	US-08-413-110-50 Sequence 50, Appl
6	31	57.4	49	1	US-08-409-442A-50 Sequence 50, Appl
7	31	57.4	49	2	US-08-469-609A-50 Sequence 50, Appl
8	31	57.4	49	2	US-09-143-190-50 Sequence 50, Appl
9	31	57.4	49	4	US-09-502-344-50 Sequence 350, App
10	31	57.4	73	1	US-08-409-442A-350 Sequence 350, App
11	31	57.4	73	2	US-08-469-609A-350 Sequence 350, App
12	31	57.4	73	3	US-09-143-190-350 Sequence 350, App
13	31	57.4	73	4	US-09-502-344-350 Sequence 350, App
14	30.8	57.0	49	1	US-08-384-541-5 Sequence 5, Appl
15	30.8	57.0	49	1	US-08-384-541-6 Sequence 6, Appl
16	30.8	57.0	49	1	US-08-384-541-7 Sequence 7, Appl
17	30.8	57.0	49	1	US-08-384-541-8 Sequence 8, Appl
18	30.8	56.3	52	4	US-09-493-491-40 Sequence 40, Appl
19	30.2	55.9	49	4	US-09-493-491-35 Sequence 35, Appl
20	30.2	55.9	62	1	US-08-345-861-1 Sequence 1, Appl
21	30	55.6	49	4	US-09-493-491-34 Sequence 34, Appl
22	29.8	55.2	50	4	US-09-493-491-28 Sequence 28, Appl
23	29.8	55.2	54	4	US-09-493-491-49 Sequence 49, Appl
24	29.6	54.8	71	4	US-09-495-152A-2 Sequence 2, Appl
25	29.6	54.8	60	1	US-08-099-867-7 Sequence 7, Appl
26	29.4	54.4	35	3	US-08-955-636-7 Sequence 1, Appl
27	29.4	54.4	49	4	US-09-710-200-1 Sequence 1, Appl

C 28	29.4	54.4	62	4	US-09-308-759A-29	Sequence 29, Appl
C 29	29.4	54.4	67	4	US-09-308-759A-49	Sequence 49, Appl
C 30	29.4	54.4	91	4	US-09-308-759A-40	Sequence 40, Appl
C 31	29.4	54.4	96	4	US-09-308-759A-36	Sequence 36, Appl
C 32	29.4	54.4	37	1	US-08-039-867-5	Sequence 5, Appl
C 33	29.4	53.7	47	1	US-08-162-836-10	Sequence 10, Appl
C 34	29.4	53.7	47	1	US-08-345-861-6	Sequence 6, Appl
C 35	29.4	53.7	47	2	US-08-479-105A-6	Sequence 6, Appl
C 36	29.4	53.7	47	4	US-09-502-966-3	Sequence 25, Appl
C 37	29.4	53.7	50	3	US-08-972-799A-25	Sequence 25, Appl
C 38	29.4	53.7	50	4	US-09-506-282-25	Sequence 25, Appl
C 39	29.4	53.7	50	5	PCT-US95-03339-25	Sequence 25, Appl
C 40	29.4	53.7	52	4	US-09-493-491-33	Sequence 33, Appl
C 41	29.4	53.7	54	4	US-09-493-491-27	Sequence 27, Appl
C 42	29.4	53.7	55	4	US-09-493-491-47	Sequence 47, Appl
C 43	29.4	53.0	79	1	US-08-099-867-3	Sequence 3, Appl
C 44	28.6	53.0	51	2	US-08-663-688A-2	Sequence 2, Appl
C 45	28.6	53.0	97	2	US-08-663-688A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-493-491-39
; Sequence 39, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; EARLIER FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-493-491-39

Query Match 59.3%; Score 32; DB 4; Length 52;
Best Local Similarity 79.2%; Pred. No. 0.0011;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 1 TAAATTATACGACTGCTATAGGAGACGACCCCTGAGGCTCAAA 48
|||||
1 TAAATTATACGACTGCTATAGGAGACCTGTCTTCAGATGAAA 48
|||||
RESULT 2
US-09-493-491-29
; Sequence 29, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; EARLIER FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1

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; SEQ ID NO 29
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-493-491-29

Query Match
Best Local Similarity 59.3%; Score 32; DB 4; Length 54;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATAGAGCTACTATAGGAGAGACTCA 32
DB 1 TAAATTAATAGAGCTACTATAGGAGAGACTCA 32

RESULT 3
US-07-931-473B-50
; Sequence 50, Application US/07931473B
; Patent No. 5270163
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/931,473B
; FILING DATE: 19920817
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-931-473B-50

Query Match
Best Local Similarity 57.4%; Score 31; DB 1; Length 49;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TATAGAGCTACTATAGGAGAGAGCTGAGGCTCAAGTCA 52
DB 1 TATAGAGCTACTATAGGAGAGAGCTGAGGCTCAAGTCA 47

RESULT 4
US-07-714-131C-50
; Sequence 50, Application US/07714131C
; Patent No. 5475096
; GENERAL INFORMATION:
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; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 344
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/714,131C
; FILING DATE: June 10, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-714-131C-50

Query Match
Best Local Similarity 57.4%; Score 31; DB 1; Length 49;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TATAGAGCTACTATAGGAGAGAGCTGAGGCTCAAGTCA 52
DB 1 TATAGAGCTACTATAGGAGAGAGCTGAGGCTCAAGTCA 47

RESULT 5
US-08-412-110-50
; Sequence 50, Application US/08412110
; Patent No. 5670637
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 344
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,110
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
```



```
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-412-110-50

Query Match
Best Local Similarity 57.4%; Score 31; DB 1; Length 49;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACGACCCCTGAGGCTCAAGTCA 52
DB 1 TAATACGACTCACTATAGGAGACGACCTTTTATCTGACAATCA 47

RESULT 6
US-08-409-442A-50
Sequence 50, Application US/08409442A
Patent No. 5696249
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,442A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-409-442A-50

Query Match
Best Local Similarity 57.4%; Score 31; DB 1; Length 49;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACGACCCCTGAGGCTCAAGTCA 52
DB 1 TAATACGACTCACTATAGGAGACGACCTTTTATCTGACAATCA 47

RESULT 7
US-08-469-609A-50
Sequence 50, Application US/08469609A
Patent No. 5843653
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,609A
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-609A-50

Query Match
Best Local Similarity 57.4%; Score 31; DB 2; Length 49;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACGACCCCTGAGGCTCAAGTCA 52
DB 1 TAATACGACTCACTATAGGAGACGACCTTTTATCTGACAATCA 47

RESULT 8
US-09-143-190-50
Sequence 50, Application US/09143190
```

Patent No. 6110900
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,190
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-143-190-50
Query Match 57.4%; Score 31; DB 3; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.0026;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TAATACGACTCTATATAGGAGCATCAGACTTTAATCTGACAAATCA 52
DB 1 TAATACGACTCTATATAGGAGCATCAGACTTTAATCTGACAAATCA 47

RESULT 9
US-09-502-344-50
Sequence 50, Application US/09502344
Patent No. 6331398
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/502,344
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-502-344-50
Query Match 57.4%; Score 31; DB 4; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.0026;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TAATACGACTCTATATAGGAGCATCAGACTTTAATCTGACAAATCA 52
DB 1 TAATACGACTCTATATAGGAGCATCAGACTTTAATCTGACAAATCA 47

RESULT 10
US-08-409-442A-350
Sequence 350, Application US/08409442A
Patent No. 5696249
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado

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1      COUNTRY: USA
2      ZIP: 80111
3      COMPUTER READABLE FORM:
4      MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
5      COMPUTER: IBM compatible
6      OPERATING SYSTEM: MS-DOS
7      SOFTWARE: Wordperfect 5.1
8      CURRENT APPLICATION DATA:
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12     APPLICATION NUMBER: 07/714,131
13     FILING DATE: June 10, 1991
14     PRIOR APPLICATION DATA: 07/536,428
15     APPLICATION NUMBER: 07/536,428
16     FILING DATE: June 11, 1990
17     ATTORNEY/AGENT INFORMATION:
18     NAME: Barry J. Swanson
19     REGISTRATION NUMBER: 33,215
20     REFERENCE/DOCKET NUMBER: NEX01/C3
21     TELECOMMUNICATION INFORMATION:
22     TELEPHONE: (303) 793-3433
23     TELEFAX: (303) 793-3433
24     INFORMATION FOR SEQ ID NO: 350:
25     SEQUENCE CHARACTERISTICS:
26     LENGTH: 73 nucleotides
27     TYPE: nucleic acid
28     STRANDEDNESS: single
29     TOPOLOGY: linear
30     US-08-409-442A-350
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33     Best Local Similarity 78.7%; Pied. No. 0.0028;
34     Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0.
35
36     QY 6 TATACGACTCCTTAGAGAGACCTAGACCCTGAGCTCAAGTCA 52
37     1 TATACGACTCCTTAGAGAGACCTAGACCCTGAGCTTATCTACATCA 47
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39     RESULT 11
40     US-08-469-609A-350
41     Sequence 350, Application US/08469609A
42     Patent No. 5843653
43     GENERAL INFORMATION:
44     APPLICANT: Larry Gold
45     APPLICANT: Craig Tuerk
46     TITLE OF INVENTION: Nucleic Acid Ligands
47     NUMBER OF SEQUENCES: 374
48     CORRESPONDENCE ADDRESS:
49     ADDRESSEE: Swanson & Bratschun, L.L.C.
50     STREET: 8400 E. Prentice Avenue, Suite 200
51     CITY: Englewood
52     STATE: Colorado
53     COUNTRY: USA
54     ZIP: 80111
55     COMPUTER READABLE FORM:
56     MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
57     COMPUTER: IBM compatible
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59     SOFTWARE: Wordperfect 5.1
60     CURRENT APPLICATION DATA:
61     APPLICATION NUMBER: US/08/469,609A
62     FILING DATE: June 6, 1995
63     PRIOR APPLICATION DATA:
64     APPLICATION NUMBER: 08/428,964
65     FILING DATE: April 25, 1995
66     PRIOR APPLICATION DATA: 08/412,110
67     APPLICATION NUMBER: 08/412,110
68     FILING DATE: March 27, 1995
69     PRIOR APPLICATION DATA:
70     APPLICATION NUMBER: 08/409,442
71     FILING DATE: March 24, 1995

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 07/714,131
3 FILING DATE: June 10, 1991
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 07/536,428
6 FILING DATE: June 11, 1990
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Barry J. Swanson
9 REGISTRATION NUMBER: 33,215
10 REFERENCE/DOCKET NUMBER: NEX01/C5
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (303) 793-3333
13 TELEFAX: (303) 793-3433
14 INFORMATION FOR SEQ ID NO: 350:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 73 nucleotides
17 TYPE: nucleic acid
18 STRANDEDNESS: single
19 TOPOLOGY: Linear
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```

NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-143-190-350

Query Match 57.4%; Score 31; DB 3; Length 73;
Best Local Similarity 76.7%; Pred. No. 0.0028;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TAAATGAGCTCATTATAGGAGACTGAGCCCTGAGGCTCAAGTCA 52
DB 1 TAAATGAGCTCATTATAGGAGACTGAGCCCTTATATCTGACAATCA 47

RESULT 13
US-09-502-344-350
Sequence 350, Application US/09502344
Patent No. 6331398
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/502,344
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-502-344-350

Query Match 57.4%; Score 31; DB 4; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.0028;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TAAATGAGCTCATTATAGGAGACTGAGCCCTGAGGCTCAAGTCA 52
DB 1 TAAATGAGCTCATTATAGGAGACTGAGCCCTTATATCTGACAATCA 47

RESULT 14
US-08-384-541-5
Sequence 5, Application US/08384541
Patent No. 5622827
GENERAL INFORMATION:
APPLICANT: McAllister, Diane L. and
APPLICANT: Clark, Kathy A.
TITLE OF INVENTION: AMPLIFICATION PRIMERS AND
TITLE OF INVENTION: NUCLEIC ACID PROBES
TITLE OF INVENTION: TARGETED TO COCCIDIOIDES
TITLE OF INVENTION: IMMUTIS NUCLEIC ACID
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,541
FILING DATE: February 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 210/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-384-541-5

Query Match 57.0%; Score 30.8; DB 1; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.0031;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

100

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 : Search time 20.6694 Seconds
(Without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-5

Perfect score: 24 GACCACTCGTGTGAACCTCCA 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents, NA.*
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6: /cgn2_6/pdata/1/ina/Backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	21	87.5	40 3	US-08-448-446B-16 Sequence 16, Appl
2	20	83.3	20 1	US-08-363-233B-5 Sequence 5, Appl
3	14	58.3	33 2	US-08-343-923-12 Sequence 12, Appl
4	14	58.3	60 4	US-09-257-581-3 Sequence 3, Appl
5	13.6	56.7	46 4	US-09-199-737-19 Sequence 19, Appl
6	13.6	56.7	46 4	US-09-058-333A-19 Sequence 19, Appl
7	13.4	55.8	32 1	US-08-868-506-10 Sequence 10, Appl
8	13.4	55.8	32 3	US-09-128-967-10 Sequence 10, Appl
9	13.4	55.8	95 4	US-09-221-298-35 Sequence 53, Appl
10	13	54.2	27 4	US-08-584-040-35 Sequence 53, Ap
11	13	54.2	27 4	US-08-584-040-35 Sequence 1969, Ap
12	13	54.2	56 1	US-08-468-674B-31 Sequence 31, Appl
13	13	54.2	56 1	US-08-780-571-31 Sequence 21, Appl
14	13	54.2	78 4	US-08-981-988A-21 Sequence 38, Appl
15	13	54.2	98 1	US-08-472-255A-38 Sequence 38, Appl
16	13	54.2	98 1	US-08-479-724A-38 Sequence 38, Appl
17	13	54.2	98 3	US-08-472-255B-38 Sequence 38, Appl
18	13	54.2	98 3	US-08-952-793-38 Sequence 38, Appl
19	13	54.2	98 5	PCT-US96-09455A-38 Sequence 38, Appl
20	12.8	53.3	20 4	US-09-161-994A-51 Sequence 21, Appl
21	12.8	53.3	24 3	US-08-641-291A-54 Sequence 54, Appl
22	12.8	53.3	27 4	US-08-623-428D-13 Sequence 13, Appl
23	12.8	53.3	37 1	US-08-061-889-3 Sequence 3, Appl
24	12.8	53.3	37 1	US-08-623-428D-7 Sequence 7, Appl
25	12.8	53.3	37 5	PCT-US94-05378-3 Sequence 3, Appl
26	12.8	53.3	45 4	US-09-266-462-10 Sequence 10, Appl
27	12.8	53.3		

28	12.8	53.3	45 4	US-09-266-462-12 Sequence 12, Appl
29	12.8	53.3	86 1	US-07-964-624D-57 Sequence 57, Appl
30	12.8	53.3	86 1	US-08-442-062-57 Sequence 57, Appl
31	12.8	53.3	86 1	US-08-748-697A-57 Sequence 57, Appl
32	12.8	53.3	86 4	US-09-165-616-57 Sequence 57, Appl
33	12.4	51.7	29 1	US-07-638-512-12 Sequence 12, Appl
34	12.4	51.7	32 1	US-08-644-664B-39 Sequence 39, Appl
35	12.4	51.7	47 2	US-08-761-277A-39 Sequence 39, Appl
36	12.4	51.7	47 4	US-09-641-638-1120 Sequence 1120, Ap
37	12.4	51.7	78 3	US-08-945-734-48 Sequence 48, Appl
38	12.4	51.7	78 4	US-09-258-797-43 Sequence 43, Appl
39	12.4	51.7	78 5	PCT-US96-09451-43 Sequence 43, Appl
40	12.2	50.8	23 5	PCT-US94-00089-5 Sequence 5, Appl
41	12.2	50.8	23 5	US-08-435-350-53 Sequence 53, Appl
42	12.2	50.8	27 1	US-08-484-661A-46 Sequence 46, Appl
43	12.2	50.8	29 3	US-08-656-664-46 Sequence 46, Appl
44	12.2	50.8	29 3	PCT-US96-09641-46 Sequence 46, Appl
45	12.2	50.8	33 3	US-08-484-661A-45 Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-448-446B-16
Sequence 16, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment of Leukemias
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESS: Kurtz Mackiewicz & No. 6080851iris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
FILING DATE: July 10, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/989,852
FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yalko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C
TELEPHONE: (215) 568-3439
FAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 40
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE:
US-08-448-446B-16
Query Match 87.5%; Score 21; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 CAACCTCGTGTGAACCTCCA 24

DB 20 CAACTGCTGTGAACTCCA 40

RESULT 2

US-08-363-233B-5

Sequence 5, Application US/08363233B
Patent No. 5714383
GENERAL INFORMATION:
APPLICANT: Thompson, James D.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
MYELOGENOUS LEUKEMIA
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,233B
FILING DATE: December 23, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
APPLICATION DATA: described below:

2

APPLICATION NUMBER: 07/882,822
FILING DATE: May 14, 1992
APPLICATION NUMBER: 08/193,922
FILING DATE: February 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-233B-5

Query Match

Best Local Similarity 83.3%; Score 20; DB 1; Length 20;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAACTGCTGTGAACTCC 23

DB 1 CAACTGCTGTGAACTCC 20

RESULT 3

US-08-343-923-12

Sequence 12, Application US/08343923
Patent No. 5856153

GENERAL INFORMATION:

APPLICANT: TIRABY, Gerard et al.
TITLE OF INVENTION: NEW SUICIDE GENES AND NEW ASSOCIATIONS
OF PYRIMIDINE NUCLEOBASE AND NUCLEOSIDE ANALOGS . . .
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSEE: LARSON AND TAYLOR
STREET: 727 SOUTH 23RD STREET
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,923
FILING DATE: 17-NOV-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: SCHULMAN, B. AARON
REGISTRATION NUMBER: 31,877
REFERENCE/DOCKET NUMBER: XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-920-7200
TELEFAX: 703-892-8428

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-343-923-12

Query Match

Best Local Similarity 58.3%; Score 14; DB 2; Length 33;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ACCAACTGCTGTGAACTCC 23

DB 9 ACCAACTGCTGTGAACTCC 30

RESULT 4

US-09-257-581-3/C

Sequence 3, Application US/09257581

Patent No. 6207419

GENERAL INFORMATION:

APPLICANT: Church, Frank C.
TITLE OF INVENTION: THROMBIN INHIBITORY AGENTS AND METHODS OF USING SAME
FILE REFERENCE: 3470-232
CURRENT APPLICATION NUMBER: US/09/257,581
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 60/076,210
EARLIER FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3

SEQUENCE: DNA

LENGTH: 60

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

Query Match

Best Local Similarity 58.3%; Score 14; DB 4; Length 60;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CAACTGCTGTGAACTCCA 24

DB 59 CAACTGCTGTGAACTCCA 38

RESULT 5


```
US-09-199-737-19/c
; Sequence 19, Application US/09199737A
; Patent No. 6287788
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; APPLICANT: Branchek, Theresa A.
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
; FILE REFERENCE: 52241-D-PCT-US
; CURRENT APPLICATION NUMBER: US/09/199,737A
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO: 19
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-199-737-19
Query Match          56.7%; Score 13.6; DB 4; Length 46;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      3  CCAACTCGTGTGTGAAGTC 22
Db      39  CCAACTCGTGTGTCAACCC 20

RESULT 6
US-09-058-333A-19/c
; Sequence 19, Application US/09058333A
; Patent No. 6368812
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,333A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 28,678
; NAME: White, John P
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 52241-E/JPM/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-058-333A-19
Query Match          56.7%; Score 13.6; DB 4; Length 46;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      3  CCAACTCGTGTGTGAAGTC 22
Db      39  CCAACTCGTGTGTCAACCC 20

RESULT 7
US-08-869-506-10
; Sequence 10, Application US/08869506
; Patent No. 5827710
; GENERAL INFORMATION:
; APPLICANT: Uchida, Kohji
; APPLICANT: Matsukawa, Hirokazu
; APPLICANT: Matuo, Yushi
; APPLICANT: Fujita, Tutosi
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 No. 5827710th Gieble Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,506
; FILING DATE: 05-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 73797/1996
; FILING DATE: 29-MAR-1996
; NAME: Crawford, Arthur R.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 159-43
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4100
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-08-869-506-10
Query Match          55.8%; Score 13.4; DB 1; Length 32;
Best Local Similarity 73.9%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY      1  GACCAACTCGTGTGTGAAGTC 23
Db      8  GCCCAACTCGTGTGTGAAGTC 30

RESULT 8
US-09-128-967-10
; Sequence 10, Application US/09128967
```

```
Patent No. 6057141
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matuo, Yushi
APPLICANT: Fujita, Tutosi
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
TITLE OF INVENTION: LACTATE DEHYDROGENASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. 6057141th Giebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/869,506
FILING DATE: 05-JUN-1997
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 159-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-09-128-967-10

Query Match          55.8%; Score 13.4; DB 3; Length 32;
Best Local Similarity 73.9%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GACCAACTGCTGTGTGAACCTC 23
      | | | | | | | | | | | | | |
DB 8 GCCCAACTGCTGTGTGAACCTC 30

RESULT 9
US-09-221-298-53/c
Sequence 53, Application US/09221298
Patent No. 6284241
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 53
LENGTH: 95
TYPE: DNA
ORGANISM: Human
```

```
FEATURE:
NAME/KEY: modified_base
LOCATION: (37)
OTHER INFORMATION: Where n is a, c, g or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (60)
OTHER INFORMATION: Where n is a, c, g or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (73)
OTHER INFORMATION: Where n is a, c, g or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (76)
OTHER INFORMATION: Where n is a, c, g or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (92)
OTHER INFORMATION: Where n is a, c, g or t
US-09-221-298-53

Query Match          55.8%; Score 13.4; DB 4; Length 95;
Best Local Similarity 73.9%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ACCAACTGCTGTGTGAACCTCA 24
      | | | | | | | | | | | | | |
DB 28 AACCAACTGCTGTGAACCTCA 6

RESULT 10
US-08-584-040-3546
Sequence 3546, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
```

TELEFAX: (213) 955-0440
TELEX: 67-3510
OTHER INFORMATION: The letter "N" represents the stem II region
of an HH ribozyme.
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OTHER INFORMATION: of an HH ribozyme.
US-08-584-040-3546

Query Match 54.2%; Score 13; DB 4; Length 27;
Best Local Similarity 59.1%; Pred. No. 5.8e+02;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 CCAACTCGTGTGGAACCTCA 24
|||||:| ||||:|
DB 5 CCAACUGAUGANGAAGAACUCCA 26

RESULT 11
US-08-584-040-4969
Sequence 4969, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Payco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4969:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:

OTHER INFORMATION: The letter "N" represents the stem II region
of an HH ribozyme.
US-08-584-040-4969

Query Match 54.2%; Score 13; DB 4; Length 27;
Best Local Similarity 59.1%; Pred. No. 5.8e+02;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 CCAACTCGTGTGGAACCTCA 24
|||||:| ||||:|
DB 5 CCAACUGAUGANGAAGAACUCCA 26

RESULT 12
US-08-468-674B-31/C
Sequence 31, Application US/08468674B
Patent No. 5639642
GENERAL INFORMATION:
APPLICANT: Kjeldsen, Thomas B
APPLICANT: Vad, Knud
TITLE OF INVENTION: SYNTHETIC LEADERS PEPTIDE SEQUENCES
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56396420 No. 5639642disk of No. 5639642th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,674B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,852
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4085,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-468-674B-31

Query Match 54.2%; Score 13; DB 1; Length 56;
Best Local Similarity 76.2%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 ACCAATCGTGTGTGGAACCTC 22
|||||:| ||||:|
DB 43 ACCAATCGTGTGTGTCTC 23

RESULT 13
US-08-780-571-31/C
Sequence 31, Application US/08780571
Patent No. 5795746
GENERAL INFORMATION:
APPLICANT: Kjeldsen, Thomas B
APPLICANT: Vad, Knud

;; TITLE OF INVENTION: SYNTHETIC LEADERS PEPTIDE SEQUENCES
;; NUMBER OF SEQUENCES: 89
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: NO. 57957460 No. 5795746disk of No. 5795746th America, Inc.
;; STREET: 405 Lexington Avenue, 64th Floor
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10174-6401
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Tape
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/780,571
;; FILING DATE: 08-JAN-1997
;; CLASSIFICATION: 435
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/468,674
;; FILING DATE: 06-JUN-1995
;; APPLICATION NUMBER: US 08/282,852
;; FILING DATE: 29-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lambiris, Elias J.
;; REGISTRATION NUMBER: 33,728
;; REFERENCE/DOCKET NUMBER: 4085,220-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 56 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; US-08-780-571-31
;;
Query Match 54.2%; Score 13; DB 1; Length 56;
Best Local Similarity 76.2%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ACCAAGCTGTGTGTAAGTC 22
DB 43 ACCAAGCTGTGTGTTCTC 23
;;
RESULT 14
US-08-981-988A-21
;; Sequence 21, Application US/08981988A
;; Patent No. 6337194
;; GENERAL INFORMATION:
;; APPLICANT: Vittal Maliya Scientific Research Foundation
;; APPLICANT: The University of Leicester
;; TITLE OF INVENTION: Insulin
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: VITTAL MALIYA SCIENTIFIC RESEARCH FOUNDATION
;; STREET: K. R. ROAD
;; CITY: BANGALORE
;; COUNTRY: INDIA
;; ZIP: 560 004
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EFO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/981,988A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIORITY APPLICATION DATA:

;; APPLICATION NUMBER: GB 9513967.1
;; FILING DATE: 08-JUL-1995
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 78 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-981-988A-21
;;
Query Match 54.2%; Score 13; DB 4; Length 78;
Best Local Similarity 76.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ACCAAGCTGTGTGTAAGTC 22
DB 12 ACCAAGCTGTGTGTTCTC 32
;;
RESULT 15
US-08-472-255A-38/C
;; Sequence 38, Application US/08472255A
;; Patent No. 576853
;; GENERAL INFORMATION:
;; APPLICANT: PARMA, DAVID
;; APPLICANT: GOLD, LARRY
;; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
;; TITLE OF INVENTION: TO SELECTINS (AS AMENDED)
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Swanson & Bratschun, L.L.C.
;; STREET: 8400 E. Prentice Avenue, Suite 200
;; CITY: Englewood
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: Wordperfect 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/472,255A
;; FILING DATE: 07-JUNE-1995
;; CLASSIFICATION: 536
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/714,131
;; FILING DATE: 10-JUNE-1991
;; PRIORITY APPLICATION DATA: 07/536,428
;; FILING DATE: 11-JUNE-1991
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/964,624
;; FILING DATE: 21-OCTOBER-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX40-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: RNA
;; FEATURE:
;; OTHER INFORMATION: All C's are 2'-NH2 cytosine
;; FEATURE:
;; OTHER INFORMATION: All U's are 2'-NH2 uracil
;; US-08-472-255A-38

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us-09-121-239-5.rni

Page 7

Query Match 54.2%; Score 13; DB 1; Length 98;
Best Local Similarity 76.2%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 2 ACCAAGCTGCTGTGAACCTC 22
| | | | | | | | | | | | | | | | | | | | | |
Db 30 ACCAAGCTGCTGTGAACCTC 10
| | | | | | | | | | | | | | | | | | | | | |
Search completed: December 21, 2002, 11:58:20
Job time : 22.6694 secs

us-09-121-239-9.rn1

Page 1

OM nucleic - nucleic search, using sw model
Run on: December 21, 2002, 02:28:32 ; Search time 21.5306 Seconds
(without alignments)
356.094 Million cell updates/sec

Title:	US-09-121-239-9
Perfect score:	25
Sequence:	1 GACTGTCCACAGCATTCGCGTACC 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues
 Annotations: 687286

Minimum	DB seq	length:	0
Maximum	DB seq	length:	100

Post-processing:	Minimum Match	0%
	Maximum Match	10%

Listing first 45 summaries

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Database : Issued_patents_NA:*
1: /cqn2_6/ptodata/1/ina/5A_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/ob-comb.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS-COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.		No.					
1	25	100.0	56	1	US-07-940-652-17	Sequence 17, Appl	
2	25	100.0	56	1	US-08-225-553-17	Sequence 17, Appl	
3	25	100.0	26	1	US-08-363-223B-6	Sequence 6, Appl	
4	24	92.0	22	1	US-08-152-621-11	Sequence 11, Appl	
5	18	72.0	22	5	PCT-US92-05035-11	Sequence 11, Appl	
6	18	72.0	62	3	US-08-448-446B-1	Sequence 1, Appl	
7	18	72.0	81	3	US-08-448-446B-2	Sequence 2, Appl	
8	18	72.0	28	4	US-09-341-955-5	Sequence 2, Appl	
9	16	64.0	28	4	US-08-477-527A-130	Sequence 130, App	
10	14.2	56.8	86	2	US-08-477-527A-139	Sequence 148, App	
11	14.2	56.8	86	2	US-08-477-527A-148	Sequence 139, App	
12	14.2	56.8	86	3	US-08-481-710-130	Sequence 148, App	
13	14.2	56.8	86	3	US-08-481-710-139	Sequence 139, App	
14	14.2	56.8	86	3	US-08-481-710-148	Sequence 139, App	
15	14.2	56.8	86	5	PCT-US96-09537-130	Sequence 148, App	
16	14.2	56.8	86	5	PCT-US96-09537-148	Sequence 19, Appl	
17	14.2	56.8	61	3	US-08-448-446B-19	Sequence 7, Appl	
18	14	56.0	61	3	US-08-482-733-7	Sequence 8, Appl	
19	13.8	55.2	33	1	US-08-462-733-8	Sequence 5, Appl	
20	13.8	55.2	33	1	US-08-462-733-5	Sequence 6, Appl	
21	13.8	55.2	33	1	US-08-453-742-6	Sequence 7, Appl	
22	13.8	55.2	33	1	US-08-176-402-7	Sequence 8, Appl	
23	13.8	55.2	33	1	US-08-176-402-0	Sequence 5, Appl	
24	13.8	55.2	33	1	US-08-454-464-6	Sequence 6, Appl	
25	13.8	55.2	33	1	US-08-454-464-6	Sequence 5, Appl	
26	13.8	55.2	33	1	US-08-453-722-5	Sequence 5, Appl	
27	13.8	55.2	33	1	US-08-453-722-5	Sequence 5, Appl	

[illegible]

ALIGNMENTS

RESULT 1
US-07-940-652-17
Sequence 17, Application US/07940652

Patent No. 5424413
GENERAL INFORMATION:
Hodan et al.

TITLE OF INVENTION: BRANCHED NO
 NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
511 West Sixth Street

CITY: Los Angeles
STATE: California

COUNTRY: USA
ZIP: 90017

```

COMPUTER: IBM compatible
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPTTFR: IBM Compatible

```

OPERATING SYSTEM: IBM AIX
; wordperfect (Version 5.1)
SOFTWARE: wordperfect (Version 5.1)
; STATISTICAL DATA:

CONTRACT NUMBER: US
APPLICATION NUMBER: 19920904
FILING DATE: 19920904

CLASSIFICATION: 455
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/07/827,021

ATTORNEY/AGENT INFORMATION: 22-JAN-1992

NAME: WALDUIG, RICHARD
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 199/201

TELECOMMUNICATION INFORMATION
TELEPHONE: (213) 489-1600

TELEFAX: (212) 512-1111
TELEX: 67-3510
TELEPHONE FOR SEO ID NO: 17

SEQUENCE CHARACTERISTICS:
LENGTH: 56

TYPE: NOCTILE
STRANDEDNESS: single
STRENGTH: linear

US-07-940-652-17

Query Match	Best Local Similarity	Best of Conservative
100.0%		

1 GACTGTCACAGCATTCGCTG

Db 3 GACTGTCACAGCATTCGGCTG

RESULT 2

US-08-255-553-17
Sequence 17, Application US/08255553
Patent No. 5451503

GENERAL INFORMATION:

APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)

APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992

APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

Query Match

Best Local Similarity 100.0%; Score 25; DB 1; Length 56;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GACTGTCCACAGCATTCGGCTGACC 25
3 GACTGTCCACAGCATTCGGCTGACC 27

RESULT 3

US-08-363-233B-6
Sequence 6, Application US/08363233B
Patent No. 5714383

GENERAL INFORMATION:

APPLICANT: Thompson, James D.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
MIELOGENOUS LEUKEMIA
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,233B
FILING DATE: December 23, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 07/882,822
FILING DATE: May 14, 1992

APPLICATION NUMBER: 08/193,922
FILING DATE: February 7, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/165

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

US-08-363-233B-6
Query Match
Best Local Similarity 96.0%; Score 24; DB 1; Length 26;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 1 GACTGTCCACAGCATTCGGCTGAC 24
3 GACTGTCCACAGCATTCGGCTGAC 26

RESULT 4

US-08-152-621-11
Sequence 11, Application US/08152621
Patent No. 5652222

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: Selective inhibition of
Leukemic Cell Proliferation by bcr-abl
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEIDEL, GONDA, LAVORGNA
ADDRESSEE: & MONACO, P.C.
STREET: 1800 Two Penn Center
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1

APPLICATION NUMBER: US/08/152,621
FILING DATE: No. 5652222 December 15, 1993

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991

ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO 56522228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-152-621-11

Query Match 72.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 CACAGCATTCGGCTGACC 25
1 CACAGCATTCGGCTGACC 18
|||||

RESULT 5
PCT-US92-05035-11
Sequence 11, Application PC/TUS9205035
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Gewirtz, Alan M.
TITLE OF INVENTION: Selective inhibition of
TITLE OF INVENTION: Leukemic cell proliferation by bcr-abl
TITLE OF INVENTION: Antisense oligonucleotides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth system of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05035
FILING DATE: 19920615
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/869,911
FILING DATE: April 14, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CTP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO 56522228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: NUCLEIC ACID
STRANDEDNESS: double stranded
TOPOLOGY: linear
PCT-US92-05035-11

Query Match 72.0%; Score 18; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 CACAGCATTCGGCTGACC 25
1 CACAGCATTCGGCTGACC 18
|||||

RESULT 6
US-08-448-446B-1
Sequence 1, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: of Leukemias
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & No. 6080851
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
FILING DATE: July 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,852
FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yalko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 62
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
US-08-448-446B-1

Query Match 72.0%; Score 18; DB 3; Length 62;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 8 CACAGCATTCGGCTGACC 25
1 CACAGCAUUDCCCGUGACC 18
|||||

RESULT 7
US-08-448-446B-2/C
Sequence 2, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: of Leukemias
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & No. 608085111s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
FILING DATE: July 10, 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,852
FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yanko Trujillo
REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 81

TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

ANTI-SENSE:
US-08-448-446B-2

Query Match 72.0%; Score 18; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 5;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CACAGCATTCGCTGACC 25
|||||
DB 81 CACAGCATTCGCTGACC 64

RESULT 8

US-09-341-955-2/c
Sequence 2, Application US/09341955
Patent No. 6251690

GENERAL INFORMATION:

APPLICANT: Kulmala, Sakari
APPLICANT: Ala-Kleme, Timo
APPLICANT: Eskola, Jarkko
APPLICANT: Korpele, Timo
TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED
FILE REFERENCE: TUR-080
CURRENT APPLICATION NUMBER: US/09/341,955
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: PCT/Fin98/00114
EARLIER FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide containing an amino group
US-09-341-955-2

Query Match 64.0%; Score 16; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 CACGATTCGCTGACC 25
|||||
DB 28 CACGATTCGCTGACC 13

RESULT 9

US-08-477-527A-130/c
Sequence 130, Application US/08477527A
Patent No. 5972599

GENERAL INFORMATION:

APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SIMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-477-527A-130

Query Match 56.8%; Score 14.2; DB 2; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Mon Dec 23 08:48:08 2002

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Page 5

OY 4 TGTCCAGACATTCGGCTG 22
|||||
Db 52 TGCCTCCGACATTCGGCTG 34

RESULT 10

US-08-477-527A-139/C
Sequence 139, Application US/08477527A
Patent No. 5972599

GENERAL INFORMATION:

APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SIMEHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
APPLICATION NUMBER: 08/117,991
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/964,624
FILING DATE: 8-SEPTEMBER-1993
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2

US-08-477-527A-139

Query Match 56.8%; Score 14.2; DB 2; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TGTCCAGACATTCGGCTG 22
|||||
Db 52 TGCCTCCGACATTCGGCTG 34

RESULT 11

US-08-477-527A-148/C
Sequence 148, Application US/08477527A
Patent No. 5972599

GENERAL INFORMATION:

APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SIMEHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
APPLICATION NUMBER: 08/117,991
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/964,624
FILING DATE: 8-SEPTEMBER-1993
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2

US-08-477-527A-148

Query Match 56.8%; Score 14.2; DB 2; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TGTCCAGACATTCGGCTG 22
|||||
Db 52 TGCCTCCGACATTCGGCTG 34

RESULT 12

US-08-481-710-130/c
; Sequence 130, Application US/08481710
; Patent No. 6028186
; GENERAL INFORMATION:
; APPLICANT: DIANE TASSET
; APPLICANT: NIKOS PAGRATIS
; APPLICANT: SUMEDHA JAYASENA
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,710
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McLearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX41-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-NH2
; US-08-481-710-130

Query Match 56.8%; Score 14.2; DB 3; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTCCACGACATTCGCTG 22
||| | |||||
DB 52 TGCCTCCGACATTCGCTG 34

RESULT 13
US-08-481-710-139/c
; Sequence 139, Application US/08481710

; Patent No. 6028186
; GENERAL INFORMATION:
; APPLICANT: DIANE TASSET
; APPLICANT: NIKOS PAGRATIS
; APPLICANT: SUMEDHA JAYASENA
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,710
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McLearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX41-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-NH2
; US-08-481-710-139

Query Match 56.8%; Score 14.2; DB 3; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTCCACGACATTCGCTG 22
||| | |||||
DB 52 TGCCTCCGACATTCGCTG 34

RESULT 14
US-08-481-710-148/c
; Sequence 148, Application US/08481710
; Patent No. 6028186
; GENERAL INFORMATION:

Mon Dec 23 08:48:08 2002

us-09-121-239-9.rml

Page 7

APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,710
FILING DATE: 7-JUNE-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: DIANE TASSET
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-481-710-148
Query Match 56.8%; Score 14.2; DB 3; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4 TGTCCACAGCATTCGCGTG 22
DB 52 TGCCCTCCGCAATTCGCGTG 34
RESULT 15
PCT-US96-09537-130/c
Sequence 130, Application PC/TUS9609537
GENERAL INFORMATION:
APPLICANT: NEXSTAR PHARMACEUTICALS, INC.
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS

APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09537
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/481,710
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: BARRY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX41/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
PCT-US96-09537-130
Query Match 56.8%; Score 14.2; DB 5; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4 TGTCCACAGCATTCGCGTG 22
DB 52 TGCCCTCCGCAATTCGCGTG 34
Search completed: December 21, 2002, 11:58:22
Job time: 23.5306 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 : Search time 17,2245 Seconds
(without alignments)
356,094 Million cell updates/sec

Title: US-09-121-239-13
Perfect score: 20
Sequence: 1 CAAGAGACAGGAGAGAG 20

Indexing table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	17.4	87.0	78	US-08-523-125-6	Sequence 6, Appl
2	17.4	87.0	78	US-08-660-561A-6	Sequence 6, Appl
3	17.4	87.0	96	US-08-523-125-9	Sequence 9, Appl
4	17.4	87.0	96	US-08-660-561A-9	Sequence 9, Appl
5	17.4	87.0	96	US-08-366-627A-8	Sequence 8, Appl
6	17.4	87.0	96	US-08-323-125-5	Sequence 5, Appl
7	14.8	74.0	66	US-08-660-561A-5	Sequence 5, Appl
8	14.8	74.0	69	US-08-523-125-7	Sequence 7, Appl
9	14.8	74.0	69	US-08-660-561A-7	Sequence 7, Appl
10	14.8	74.0	84	US-08-523-125-8	Sequence 8, Appl
11	14.8	74.0	84	US-08-660-561A-8	Sequence 8, Appl
12	14.8	74.0	87	US-08-366-627A-7	Sequence 7, Appl
13	14.8	74.0	87	US-08-523-125-10	Sequence 10, Appl
14	14.8	74.0	87	US-08-660-561A-10	Sequence 10, Appl
15	14.8	74.0	87	US-09-366-627A-9	Sequence 9, Appl
16	14.2	71.0	21	US-09-109-663-48	Sequence 48, Appl
17	14.2	71.0	45	US-08-065-844A-14	Sequence 14, Appl
18	13.8	69.0	51	US-08-171-383A-5	Sequence 5, Appl
19	13.8	69.0	51	US-08-461-041-5	Sequence 5, Appl
20	13.8	69.0	59	US-08-313-127A-2	Sequence 2, Appl
21	13.8	69.0	66	US-08-313-127A-1	Sequence 1, Appl
22	13.8	69.0	68	US-08-313-127A-4	Sequence 4, Appl
23	13.8	69.0	68	US-08-313-127A-6	Sequence 6, Appl
24	13.8	69.0	75	US-08-313-127A-8	Sequence 8, Appl
25	13.8	69.0	75	US-08-313-127A-3	Sequence 3, Appl
26	13.8	69.0	75	US-08-313-127A-5	Sequence 5, Appl
27	13.8	69.0	75	US-08-313-127A-7	Sequence 7, Appl

28	13.6	68.0	30	4	US-09-674-460-2	Sequence 2, Appl
29	13.6	68.0	82	2	US-08-051-962-7	Sequence 7, Appl
30	13.6	68.0	89	2	US-08-461-658B-42	Sequence 42, Appl
31	13.6	68.0	89	2	US-08-477-504A-42	Sequence 42, Appl
32	13.6	68.0	89	2	US-08-466-756A-42	Sequence 42, Appl
33	13.6	68.0	89	2	US-08-485-862B-42	Sequence 42, Appl
34	13.6	68.0	89	3	US-08-787-739-42	Sequence 42, Appl
35	13.6	68.0	89	3	US-08-487-077A-42	Sequence 42, Appl
36	13.6	68.0	89	3	US-08-485-863A-42	Sequence 42, Appl
37	13.6	68.0	89	4	US-08-485-049D-42	Sequence 42, Appl
38	13.6	68.0	89	4	US-09-178-115-42	Sequence 42, Appl
39	13.6	68.0	89	4	US-09-177-776-42	Sequence 42, Appl
40	13.4	67.0	20	4	US-09-658-687A-82	Sequence 82, Appl
41	13.2	66.0	71	4	US-09-363-939A-30	Sequence 30, Appl
42	13.2	66.0	71	4	US-09-363-939A-43	Sequence 43, Appl
43	13.2	66.0	85	4	US-09-051-962-9	Sequence 9, Appl
44	12.6	64.0	20	2	US-08-788-750-4	Sequence 4, Appl
45	12.6	64.0	20	3	US-08-765-340-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-523-125-6
Sequence 6, Application US/08523125
Patent No. 5830866
GENERAL INFORMATION:
APPLICANT: Redel, Eva
APPLICANT: Aird, Fraser
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5830866ris
Street: One Liberty Place - 1700 Market Street
City: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-523-125-6
Query Match 87.0%; Score 17.4; DB 2; Length 78;
Best Local Similarity 94.7%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAG 19
|||||
DB 19 CAAAGAGCTGGGAGAGAG 37

RESULT 2

US-08-660-561A-6
Sequence 6, Application US/08660561A
Patent No. 6039956

GENERAL INFORMATION:

APPLICANT: Redel, Eva
APPLICANT: Aird, Fraser
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pantlich Schwarze Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A
FILING DATE: 17-JUN-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-660-561A-6

Query Match 87.0%; Score 17.4; DB 3; Length 78;
Best Local Similarity 94.7%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAG 19
|||||
DB 19 CAAAGAGCTGGGAGAGAG 37

RESULT 3

US-08-523-125-9

Sequence 9, Application US/08523125
Patent No. 5830866

GENERAL INFORMATION:

APPLICANT: Redel, Eva
APPLICANT: Aird, Fraser
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s
STREET: One Liberty Place - 1700 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-523-125-9

Query Match 87.0%; Score 17.4; DB 2; Length 96;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAG 19
|||||
DB 37 CAAAGAGCTGGGAGAGAG 55

RESULT 4

US-08-660-561A-9
Sequence 9, Application US/08660561A
Patent No. 6039956

GENERAL INFORMATION:

APPLICANT: Redel, Eva
APPLICANT: Aird, Fraser
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pantlich Schwarze Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A
FILING DATE: 17-JUN-96
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-660-561A-9

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 3; Length 96;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGGAAG 19
DB 37 CAAGAGCAGCAGGAAG 55

RESULT 5
US-09-366-627A-8
Sequence 8, Application US/0936627A
Patent No. 6348571
GENERAL INFORMATION:
APPLICANT: REDEL, Eva
TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF USING SAME
FILE REFERENCE: 0054-103
CURRENT APPLICATION NUMBER: US/09/366,627A
PRIORITY FILING DATE: 2001-06-20
PRIORITY APPLICATION NUMBER: 09/366,627
PRIORITY FILING DATE: 1996-06-07
PRIORITY APPLICATION NUMBER: 08/523,125
PRIORITY FILING DATE: 1995-09-08
PRIORITY APPLICATION NUMBER: 08/304,383
PRIORITY FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 8
LENGTH: 96
TYPE: DNA
ORGANISM: Homo sapiens
US-09-366-627A-8

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 4; Length 96;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGGAAG 19
DB 37 CAAGAGCAGCAGGAAG 55

RESULT 6
US-08-523-125-5
Sequence 5, Application US/08523125
Patent No. 5830866
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF USING SAME
FILE REFERENCE: 0054-103
CURRENT APPLICATION NUMBER: US/08/523,125
PRIORITY FILING DATE: 2001-06-20
PRIORITY APPLICATION NUMBER: 09/366,627
PRIORITY FILING DATE: 1996-06-07
PRIORITY APPLICATION NUMBER: 08/523,125
PRIORITY FILING DATE: 1995-09-08
PRIORITY APPLICATION NUMBER: 08/304,383
PRIORITY FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 8
LENGTH: 96
TYPE: DNA
ORGANISM: Homo sapiens
US-08-523-125-5

TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s
STREET: One Liberty Place - 1700 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-523-125-5

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 2; Length 66;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGGAAG 18
DB 19 CAAGAGCAGCAGGAAG 36

RESULT 7
US-08-660-561A-5
Sequence 5, Application US/08660561A
Patent No. 6039956
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Panlitch Schwarz Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A

FILING DATE: 17-JUN-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-660-561A-5

Query Match 74.0%; Score 14.8; DB 3; Length 66;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGAGCAGGAGAA 18
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Db 19 CAAGAGAGCTGGAGAA 36

RESULT 8
US-08-523-125-7
Sequence 7, Application US/08523125
Patent No. 5830866
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s
STREET: One Liberty Place - 1700 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-523-125-7

Query Match 74.0%; Score 14.8; DB 2; Length 69;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGAGCAGGAGAA 18
|||||
Db 19 CAAGAGAGCTGGAGAA 36

RESULT 9
US-08-660-561A-7
Sequence 7, Application US/08660561A
Patent No. 6039956
GENERAL INFORMATION:
APPLICANT: Redel, Eva

TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paulich Schwarze Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,561A

FILING DATE: 17-JUN-96

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/304,383

FILING DATE: 12-SEP-94

CLASSIFICATION: 514

APPLICATION NUMBER: 08/523,125

FILING DATE: 08-SEP-95

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Doyle Leary, Ph.D., J.D.

REGISTRATION NUMBER: 36,317

REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-567-2020

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 69 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-660-561A-7

Query Match 74.0%; Score 14.8; DB 3; Length 69;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGAGCAGGAGAA 18
|||||
Db 19 CAAGAGAGCTGGAGAA 36

RESULT 10
US-08-523-125-8
Sequence 8, Application US/08523125
Patent No. 5830866
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830866rls
STREET: One Liberty Place - 1700 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-523-125-8
Query Match 74.0%; Score 14.8; DB 2; Length 84;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
QY 1 CAAAGGACGAGGAGAA 18
DB 37 CAAAGGACGAGGAGAA 54
RESULT 11
US-08-660-561A-8
Sequence 8, Application US/08660561A
Patent No. 6039956
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pantich Schwarz Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA

COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A
FILING DATE: 17-JUN-96
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-660-561A-8
Query Match 74.0%; Score 14.8; DB 3; Length 84;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
QY 1 CAAAGGACGAGGAGAA 18
DB 37 CAAAGGACGAGGAGAA 54
RESULT 12
US-09-366-627A-7
Sequence 7, Application US/09366627A
Patent No. 6348571
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF USING S
FILE REFERENCE: 0054-103
CURRENT APPLICATION NUMBER: US/09/366,627A
PRIORITY FILING DATE: 2001-06-20
PRIORITY FILING DATE: 09/366,627
PRIORITY FILING DATE: 1996-06-07
PRIORITY FILING DATE: 08/523,125
PRIORITY FILING DATE: 1995-09-08
PRIORITY FILING DATE: 08/304,383
PRIORITY FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 84
TYPE: DNA
ORGANISM: Rattus sp.
US-09-366-627A-7
Query Match 74.0%; Score 14.8; DB 4; Length 84;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
QY 1 CAAAGGACGAGGAGAA 18

Mon Dec 23 08:47:54 2002

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Page 6

DB 37 CAAAGAACCTGGGAGAA 54

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|||||
RESULT 13
US-08-523-125-10
; Sequence 10, Application US/08523125
; Patent No. 5830866
; GENERAL INFORMATION:
; APPLICANT: Redel, Eva
; TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s
; STREET: One Liberty Place - 1700 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,125
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/304,383
; FILING DATE: 12-SEP-94
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn Leary, Ph.D.
; REGISTRATION NUMBER: 36,317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-523-125-10

Query Match 74.0%; Score 14.8; DB 2; Length 87;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGACGACGAGGAGAA 18
DB 37 CAAAGAACCTGGGAGAA 54

RESULT 14
US-08-660-561A-10
; Sequence 10, Application US/08660561A
; Patent No. 6039956
; GENERAL INFORMATION:
; APPLICANT: Redel, Eva
; TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Paulich Schwarze Jacobs & Nadel
; STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
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CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,561A
; FILING DATE: 17-JUN-96
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/304,383
; FILING DATE: 12-SEP-94
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/523,125
; FILING DATE: 08-SEP-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn Doyle Leary, Ph.D., J.D.
; REGISTRATION NUMBER: 36,317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-660-561A-10
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Query Match 74.0%; Score 14.8; DB 3; Length 87;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGACGACGAGGAGAA 18
DB 37 CAAAGAACCTGGGAGAA 54
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RESULT 15
US-09-366-627A-9
; Sequence 9, Application US/09366627A
; Patent No. 6348571
; GENERAL INFORMATION:
; APPLICANT: Redel, Eva
; TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF USING S
; FILE REFERENCE: 0054-1103
; CURRENT APPLICATION NUMBER: US/09/366,627A
; CURRENT FILING DATE: 2001-06-20
; PRIORITY APPLICATION NUMBER: 09/366,627
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: 08/523,125
; PRIOR FILING DATE: 1995-09-08
; PRIOR APPLICATION NUMBER: 08/304,383
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Mus sp.
; US-09-366-627A-9

Query Match 74.0%; Score 14.8; DB 4; Length 87;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Mon Dec 23 08:47:54 2002

us-09-121-239-13.rni

Page 7

OY 1 CAAGGACGAGGAGAA 18
| | | | | | | | | | | | | | | | | |
Db 37 CAAGGAGCTGGGAGAA 54

Search completed: December 21, 2002, 11:58:22
Job time : 17.2245 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 ; Search time 20.6694 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-16

Sequence: 24
1 GTGACATGAGCCCTTCAGCG 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued_Patents_NA.*
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2: /cgn2_6/plodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/plodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/plodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/plodata/1/ina/PC109.COMB.seq.*
6: /cgn2_6/plodata/1/ina/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15.8	65.8	56 1	US-07-940-652-14 Sequence 14, Appl
2	15.8	65.8	56 1	US-08-255-553-14 Sequence 14, Appl
3	15.6	65.0	29 4	US-09-125-891-7 Sequence 7, Appl
4	15.6	65.0	35 3	US-09-329-418-27 Sequence 27, Appl
5	15.6	65.0	35 4	US-09-531-914-27 Sequence 27, Appl
6	15.4	64.2	23 1	US-08-363-233B-22 Sequence 21, Appl
7	15.4	64.2	23 1	US-08-448-446B-1 Sequence 22, Appl
8	15.4	64.2	62 3	US-08-448-446B-1 Sequence 1, Appl
9	15.4	64.2	62 3	US-08-793-408-9 Sequence 1, Appl
10	15.4	64.2	62 3	US-08-793-408-9 Sequence 1, Appl
11	15.4	64.2	62 3	US-09-139-762A-11 Sequence 9, Appl
12	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
13	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
14	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
15	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
16	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
17	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
18	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
19	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
20	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
21	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
22	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
23	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
24	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
25	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
26	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl
27	15.4	64.2	62 3	US-09-139-762A-11 Sequence 11, Appl

C	28	14.2	59.2	23	4	US-09-634-262-26	Sequence 26, Appl
	29	14.2	59.2	23	1	US-08-363-233B-24	Sequence 24, Appl
	30	14.2	59.2	23	1	US-08-363-233B-25	Sequence 25, Appl
	31	14.2	59.2	26	1	US-08-152-621-33	Sequence 33, Appl
	32	14.2	59.2	26	4	US-09-341-955-1	Sequence 1, Appl
	33	14.2	59.2	26	5	PCT-US92-05035-13	Sequence 33, Appl
	34	14.2	59.2	26	5	PCT-US93-07541-25	Sequence 25, Appl
	35	14.2	59.2	32	3	US-08-946-914-57	Sequence 57, Appl
	36	14.2	59.2	32	4	US-08-656-450-57	Sequence 57, Appl
	37	14.2	59.2	42	2	US-08-768-177-3	Sequence 3, Appl
	38	14.2	59.2	42	4	US-08-991-675A-3	Sequence 3, Appl
	39	14.2	59.2	56	1	US-07-940-652-19	Sequence 19, Appl
	40	14.2	59.2	56	1	US-08-255-553-19	Sequence 19, Appl
	41	13.6	56.7	32	2	US-08-706-037-12	Sequence 12, Appl
	42	13.6	56.7	32	2	US-09-005-397-12	Sequence 12, Appl
	43	13.6	56.7	60	4	US-09-128-354-20	Sequence 20, Appl
	44	13.4	55.8	23	1	US-08-399-675-15	Sequence 15, Appl
	45	13.4	55.8	23	3	US-08-281-203-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-07-940-652-14/c
; Sequence 14, Application US/07940652
; Patent No. 5424413
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan et al.
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,652
; FILING DATE: 19920904
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/827,021
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Walburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 199/201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 14:
; LENGTH: 56
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-940-652-14
Query Match 65.8% Score 15.8; DB 1; Length 56;
Best Local Similarity 89.5% Pred. No. 83;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 ACATGAAGCCCTTCAGCG 24
DB 35 ACATGAAGCCCTTCAGCG 17

RESULT 2

US-08-255-553-14/c
; Sequence 14, Application US/08255553
; Patent No. 5451503

GENERAL INFORMATION:

APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

SEQUENCE CHARACTERISTICS:

LENGTH: 56
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-255-553-14

Query Match

Best Local Similarity 65.8%; Score 15.8; DB 1; Length 56;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 ACATGAGCCCTTCAGCG 24
DB 35 ACCTAAGCCCTTCAGCG 17

RESULT 3

US-09-125-891-7
; Sequence 7, Application US/09125891
; Patent No. 6462185

GENERAL INFORMATION:

APPLICANT: TAKAKURA, Yoshimitsu
APPLICANT: INOUE, Tsuyoshi
APPLICANT: SAITO, Hideaki
APPLICANT: ITO, Toru

TITLE OF INVENTION: Flower Organ-Specific Gene and Its Promoter Sequence

FILE REFERENCE: 0230-0125P
CURRENT APPLICATION NUMBER: US/09/125,891
CURRENT FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: PCT/JP97/04892
EARLIER FILING DATE: 1997-12-26
EARLIER APPLICATION NUMBER: 349505/1996 JAPAN
EARLIER FILING DATE: 1996-12-27

NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: plasmid psp24
US-09-125-891-7

Query Match

Best Local Similarity 65.0%; Score 15.6; DB 4; Length 29;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TGGAACATGAGCCCTTCAGCG 23
DB 5 TAGAACATGAGCTTCAGCG 26

RESULT 4

US-09-329-418-27/c
; Sequence 27, Application US/09329418
; Patent No. 6096539

GENERAL INFORMATION:

APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer

US-09-329-418-27

Query Match

Best Local Similarity 65.0%; Score 15.6; DB 3; Length 35;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GGAACATGAGCCCTTCAGCG 24
DB 35 GGAACCAAGTCCTTAAGCG 14

RESULT 5

US-09-531-914-27/c
; Sequence 27, Application US/09531914
; Patent No. 6267956

GENERAL INFORMATION:

APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/531,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
PRIOR FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer

US-09-531-914-27

Query Match
Best Local Similarity 65.0%; Score 15.6; DB 4; Length 35;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 11

US-09-139-762A-9
 ; Sequence 9, Application US/09139762A
 ; Patent No. 6013453
 ; GENERAL INFORMATION:
 ; APPLICANT: Choo, Yen
 ; APPLICANT: Kluug, Aaron
 ; APPLICANT: Sanchez Garcia, Isidro
 ; TITLE OF INVENTION: Improvements in or relating to
 ; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
 ; NUMBER OF SEQUENCES: 125
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/139,762A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/793,408
 ; FILING DATE: 02-JUN-1997
 ; APPLICATION NUMBER: PCT/GB95/01949
 ; FILING DATE: 17-AUG-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9514698.1
 ; FILING DATE: 18-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9422534.9
 ; FILING DATE: 08-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9416880.4
 ; FILING DATE: 20-AUG-1994
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-139-762A-9
 ; Query Match 62.5%; Score 15; DB 3; Length 33;
 ; Best Local Similarity 100.0%; Pred. No. 1.Be+02;
 ; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; QY 10 GAAGCCTTCAGCGG 24
 ; DB 16 GAAGCCTTCAGCGG 30
 ; RESULT 12
 ; US-09-139-762A-11
 ; Sequence 11, Application US/09139762A
 ; Patent No. 6013453
 ; GENERAL INFORMATION:
 ; APPLICANT: Choo, Yen
 ; APPLICANT: Kluug, Aaron
 ; APPLICANT: Sanchez Garcia, Isidro
 ; TITLE OF INVENTION: Improvements in or relating to
 ; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
 ; NUMBER OF SEQUENCES: 125
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.

COUNTRY: USA
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/139,762A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/793,408
 FILING DATE: 02-JUN-1997
 APPLICATION NUMBER: PCT/GB95/01949
 FILING DATE: 17-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9514698.1
 FILING DATE: 18-JUL-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9422534.9
 FILING DATE: 08-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9416880.4
 FILING DATE: 20-AUG-1994
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-09-139-762A-11
 ; Query Match 62.5%; Score 15; DB 3; Length 33;
 ; Best Local Similarity 100.0%; Pred. No. 1.Be+02;
 ; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; QY 10 GAAGCCTTCAGCGG 24
 ; DB 16 GAAGCCTTCAGCGG 30
 ; RESULT 13
 ; US-08-706-037-14
 ; Sequence 14, Application US/08706037
 ; Patent No. 5770419
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Feng
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Wahleithner, Jill A.
 ; TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
 ; TITLE OF INVENTION: ENHANCED ACTIVITY
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 57704190 No. 5770419disk of No. 5770419th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/706,037
 ; FILING DATE: 30-AUG-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/002,800
 ; FILING DATE: 1-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:

NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-706-037-14

Query Match 62.5%; Score 15; DB 1; Length 34;
Best Local Similarity 78.3%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAACATGAGCCCTTCAGCG 24
DB 10 TGATGATGAGCTTCATCAG 32

RESULT 14
US-09-005-397-14
Sequence 14, Application US/09005397
Patent No. 5972670
GENERAL INFORMATION:
APPLICANT: Xu, Feng
APPLICANT: Berk, Randy M.
APPLICANT: Wahleithner, Jill A.
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59726700 No. 5972670disk of No. 5972670th America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005.397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/706,037
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-005-397-14

Query Match 62.5%; Score 15; DB 2; Length 34;

Best Local Similarity 78.3%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAACATGAGCCCTTCAGCG 24
DB 10 TGATGATGAGCTTCATCAG 32

RESULT 15
US-08-448-446B-12
Sequence 12, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
FILING DATE: July 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,852
FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yalko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 47
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: linear
ANTI-SENSE:
US-08-448-446B-12

Query Match 62.5%; Score 15; DB 3; Length 47;
Best Local Similarity 86.7%; Pred. No. 1.9e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 GAAGCCCTTCAGCG 24
DB 16 GAAGCCCTTCAGCG 30

Search completed: December 21, 2002, 11:58:23
Job time: 21.6694 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 ; Search time 23.2531 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-22

Sequence: 1 TGTGACTTGTGAGCTCAGGCTCTGAGT 27

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTOTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	26	96.3	80 1	US-08-152-621-7
2	26	96.3	80 1	US-08-306-6918-38
3	26	96.3	80 5	PCT-US92-05035-7
4	22	81.5	22 1	US-08-013-4193-7
5	22	81.5	22 1	US-08-122-7958-10
6	22	81.5	22 1	US-08-523-818-1
7	22	81.5	22 2	US-09-028-184-1
8	22	81.5	22 5	PCT-US94-00680-1
9	22	81.5	22 5	PCT-US94-09963A-10
10	17	63.0	56 1	US-07-940-652-19
11	17	63.0	56 1	US-08-255-553-19
12	15.8	57.8	20 1	US-07-872-678A-13
13	15.6	57.8	67 1	US-08-170-095B-35
14	15.6	57.8	80 3	US-08-921-887-48
15	15.6	57.8	20 1	US-08-761-131-7
16	15	55.6	21 3	US-07-784-222-2
17	15	55.6	27 3	US-08-998-099-78
18	15	55.6	40 1	US-08-761-131-1
19	15	55.6	40 1	US-08-584-040-1123
20	14.6	53.3	27 4	US-08-985-162-994
21	14.4	53.3	27 4	US-08-584-040-1204
22	14.4	53.3	37 1	US-08-428-733A-7
23	14.4	53.3	37 1	US-08-428-733A-38
24	14.4	53.3	37 1	US-08-428-733A-39
25	14.4	53.3	43 3	US-08-732-708C-6
26	14.4	53.3	43 3	US-08-463-224-61
27	14.2	52.6	33 1	US-08-463-224-61

28	14.2	52.6	33 2	US-08-463-377-61	Sequence 61, Appl
29	14.2	52.6	36 2	US-08-292-620A-1109	Sequence 1109, Ap
30	14.2	52.6	36 3	US-09-071-845-1109	Sequence 4, Appl1
31	14.2	52.6	41 1	US-08-654-773-4	Sequence 4, Appl1
32	14.2	52.6	41 2	US-08-909-768-4	Sequence 17, Appl
33	14.2	52.6	42 1	US-07-834-539A-17	Sequence 25, Appl
34	14.2	52.6	42 1	US-08-645-641-25	Sequence 25, Appl
35	14.2	52.6	42 1	US-08-053-131-25	Sequence 25, Appl
36	14.2	52.6	42 1	US-07-853-408B-25	Sequence 25, Appl
37	14.2	52.6	42 1	US-08-096-762-25	Sequence 17, Appl
38	14.2	52.6	42 2	US-08-800-353-17	Sequence 17, Appl
39	14.2	52.6	42 2	US-08-308-865-25	Sequence 17, Appl
40	14.2	52.6	42 4	US-08-758-417A-17	Sequence 41, Appl
41	14.2	52.6	42 5	PCT-US92-06183-17	Sequence 25, Appl
42	14.2	52.6	42 5	PCT-US92-10983-25	Sequence 122, App
43	14.2	52.6	69 1	US-08-434-001-122	Sequence 122, App
44	14.2	52.6	69 1	US-08-433-585-122	Sequence 122, App
45	14.2	52.6	69 1	US-08-433-585-122	Sequence 122, App

ALIGNMENTS

RESULT 1
US-08-152-621-7
Sequence 7, Application US/08452621
Patent No. 5652222
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: Selective Inhibition of
Leukemic Cell Proliferation by bcr-abl
TITLE OF INVENTION: Antisense Oligonucleotides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: SETDEL, GONDA, LAVORGINA
STREET: 1800 Two Penn Center
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,621
FILING DATE: No. 5652222ember 15, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monico, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
TELEPHONE: (215) 568-8983
TELEFAX: (215) 568-5549
TELEX: No. 5652222e
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-152-621-7
Query Match
Best Local Similarity 100.0%; DB 1; Length 80;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
|||||
DB 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 2

US-08-306-691B-38
Sequence 38, Application US/08306691B
Patent No. 5734039

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno

APPLICANT: Skorski, Tomasz

TITLE OF INVENTION: ANTISENSE

TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.

STREET: Two Penn Center, Suite 1800

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,691B

FILING DATE: September 15, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8321-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5734039e

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-306-691B-38

PCT-0592-05035-7

Sequence 7, Application PC/TUS9205035

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno

APPLICANT: Gewirtz, Alan M.

TITLE OF INVENTION: Selective inhibition of

TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University - Of The Common-

ADDRESSER: Wealth System of Higher Education

STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05035

FILING DATE: 19920615

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/718,302

FILING DATE: June 18, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/869,911

FILING DATE: April 14, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: None

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 Nucleotides

TYPE: NUCLEIC ACID

STRANDEDNESS: single stranded

TOPOLOGY: linear

PCT-0592-05035-7

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
|||||
DB 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 4

US-08-013-419-1/c

Sequence 1, Application US/08013419

Patent No. 530635

GENERAL INFORMATION:

APPLICANT: Macfarlane, Donald E.

TITLE OF INVENTION: Product and Process for Isolating RNA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Center, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/013,419

FILING DATE: 19930201

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: URIF1USA

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-013-419-1

Query Match 81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTTGAGCCTCAGGGCTCTGA 25
DB 22 GACTTTGAGCCTCAGGGCTCTGA 1

RESULT 5

US-08-122-795B-10/c
Sequence 10, Application US/08122795B
Patent No. 5635385
GENERAL INFORMATION:
APPLICANT: Lance H. Leopold
APPLICANT: Scott K. Shore
APPLICANT: Moole V. R. Reddy
APPLICANT: E. Premkumar Reddy
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna
ADDRESSEE: 6 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,795B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5635385e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-122-795B-10

Query Match 81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTTGAGCCTCAGGGCTCTGA 25
DB 22 GACTTTGAGCCTCAGGGCTCTGA 1

RESULT 6
US-08-525-818-1/c
Sequence 1, Application US/08525818
Patent No. 5728822

GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and Methods
TITLE OF INVENTION: of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,818
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/113,727
FILING DATE:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIFPLUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-525-818-1

Query Match 81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTTGAGCCTCAGGGCTCTGA 25
DB 22 GACTTTGAGCCTCAGGGCTCTGA 1

RESULT 7
US-09-028-184-1/c
Sequence 1, Application US/09028184
Patent No. 5985572
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and
TITLE OF INVENTION: Methods of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028.184
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525.818
FILING DATE: 07-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113.727
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013.419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kodoff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: UIRFICUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-09-028-184-1

Query Match 81.5%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTCGA 25
DB 22 GACTTGAGCCTCAGGCTCGA 1

RESULT 8
PCT-US94-00680-1/c
Sequence 1, Application PC/TUS9400680
GENERAL INFORMATION:
APPLICANT: University of Iowa, Research Foundation
TITLE OF INVENTION: Quaternary Amine Surfactants and
METHOD OF INVENTION: Methods of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00680
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013.419
FILING DATE: 01-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113.727
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIRFAPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US94-00680-1

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTCGA 25
DB 22 GACTTGAGCCTCAGGCTCGA 1

RESULT 9
PCT-US94-09963A-10/c
Sequence 10, Application PC/TUS9409963A
GENERAL INFORMATION:
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
METHOD OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna
STREET: 6 Monaco, P.C.
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09963A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122.795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
PCT-US94-09963A-10

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTCTGA 25
|||||

Db 22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 10
US-07-940-652-19
Sequence 19, Application US/07940652
Patent No. 5424413
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 19920904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear

US-07-940-652-19

Query Match 63.0%; Score 17; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
|||||

Db 40 TCTGACTTGAGCCTCA 56

RESULT 11
US-08-255-553-19
Sequence 19, Application US/0825553
Patent No. 5451503
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-255-553-19

Query Match 63.0%; Score 17; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
|||||

Db 40 TCTGACTTGAGCCTCA 56

RESULT 12
US-07-872-678A-13/C
Sequence 13, Application US/07872678A
Patent No. 5541060
GENERAL INFORMATION:
APPLICANT: Bell, Graeme, et al.
TITLE OF INVENTION: DETECTION OF EARLY-ONSET
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: Post Office Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,678A
FILING DATE: 22-APRIL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: ARCD016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924

;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-07-872-678A-13

Query Match 58.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 TTGAGCCTCAGGCTCTCA 25
|||||
Db 19 TTGAGCCTCAGAACTCTCA 1

RESULT 13
-08-170-095B-35
Sequence 35, Application US/08170095B
Patent No. 5563254

GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Blood Substitutes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Somatogen, Inc.
STREET: 2545 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,095B
FILING DATE: December 20, 1993
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: No. 5563254ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown to applicant
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: beta globin sequence fragment
HYPOTHETICAL: no
US-08-170-095B-35

Query Match 57.8%; Score 15.6; DB 1; Length 67;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 18; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 TGACTTTGAGCCTCAGGCTGTAG 26
|||||
Db 44 TGCTAGSAGCCTCAGAGTCTGAG 67

RESULT 14
US-08-921-887-48
Sequence 48, Application US/08921887
Patent No. 6030771

;; GENERAL INFORMATION:
;; APPLICANT: KHUDYAKOV, YURI E.
;; APPLICANT: FIELDS, HOWARD A.
;; TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION
;; TITLE OF INVENTION: ENDONULEASE ASSISTED LIGATION METHOD FOR MAKING THE SAME
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: JONES & ASKEW, LLP
;; STREET: 191 Peachtree Street, N.W., 37th Floor
;; CITY: Atlanta
;; STATE: GA
;; COUNTRY: USA

ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,887
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: WARREN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 03063-0380
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis virus
US-08-921-887-48

Query Match 57.8%; Score 15.6; DB 3; Length 80;
Best Local Similarity 81.8%; Pred. No. 93;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CTGACTTTGAGCCTCAGGCTCT 23
|||||
Db 59 CTGAGTCTGAGCCTCAGGCTTGT 80

RESULT 15
US-08-761-131-7/c
Sequence 7, Application US/08761131
Patent No. 5804384

GENERAL INFORMATION:
APPLICANT: M Iler, Uwe R. et al.
TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vysis, Inc.
STREET: 3100 Woodcreek Drive
CITY: Downers Grove
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60515

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

Mon Dec 23 08:47:58 2002

us-09-121-239-22.rni

Page 7

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? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/761,131
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Galloway, No. 5804384val B.
? REGISTRATION NUMBER: 33,595
? REFERENCE/DOCKET NUMBER: 01886/064001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 708-271-7417
? TELEFAX: 708-271-7048
? TELEX: 200154
? INFORMATION FOR SEO, ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: Genomic DNA
? US-08-761-131-7

Query Match 55.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACCTTTGAGCCT 15
   |||||
Db 15 TCTGACCTTTGAGCCT 1

```



7
4
1
1

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 ; Search time 23.2531 Seconds
(without alignments)
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Title: US-09-121-239-23

Sequence: 1 UCGAGCUUGAGCCUGAGCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	26	96.3	80 1	US-08-152-621-7 Sequence 7, Appl
2	26	96.3	80 1	US-08-306-6918-38 Sequence 38, Appl
3	26	96.3	80 5	PCT-US92-05035-7 Sequence 7, Appl
4	22	81.5	22 1	US-08-013-419-1 Sequence 1, Appl
5	22	81.5	22 1	US-08-123-795B-10 Sequence 10, Appl
6	22	81.5	22 1	US-08-525-818-1 Sequence 1, Appl
7	22	81.5	22 1	US-09-028-184-1 Sequence 1, Appl
8	22	81.5	22 5	PCT-US94-0963A-10 Sequence 10, Appl
9	22	81.5	22 5	PCT-US94-0963A-10 Sequence 10, Appl
10	17	63.0	56 1	US-07-940-652-19 Sequence 19, Appl
11	17	63.0	56 1	US-07-940-652-19 Sequence 19, Appl
12	15.8	57.8	20 1	US-08-255-553-19 Sequence 19, Appl
13	15.6	57.8	67 1	US-07-872-678A-13 Sequence 13, Appl
14	15.6	57.8	80 3	US-08-921-887-48 Sequence 48, Appl
15	15.6	57.8	20 1	US-08-761-131-7 Sequence 7, Appl
16	15.6	57.8	20 1	US-08-761-131-7 Sequence 7, Appl
17	15.6	57.8	20 1	US-08-761-131-7 Sequence 7, Appl
18	15.6	57.8	20 1	US-08-761-131-7 Sequence 7, Appl
19	15.6	57.8	20 1	US-08-761-131-7 Sequence 7, Appl
20	15.6	57.8	20 1	US-08-761-131-7 Sequence 7, Appl
21	14.4	53.3	27 4	US-08-584-040-3123 Sequence 1123, Ap
22	14.4	53.3	27 4	US-08-985-162-994 Sequence 994, Ap
23	14.4	53.3	27 4	US-08-584-040-3204 Sequence 3204, Ap
24	14.4	53.3	37 1	US-08-428-733A-7 Sequence 7, Appl
25	14.4	53.3	37 1	US-08-428-733A-38 Sequence 38, Appl
26	14.4	53.3	37 1	US-08-428-733A-39 Sequence 39, Appl
27	14.2	52.6	43 3	US-08-732-708C-6 Sequence 61, Appl

28	14.2	52.6	33 2	US-08-463-377-61 Sequence 61, Appl
29	14.2	52.6	36 2	US-08-292-620A-1109 Sequence 1109, Ap
30	14.2	52.6	36 3	US-09-071-845-1109 Sequence 1109, Ap
31	14.2	52.6	41 1	US-08-654-773-4 Sequence 4, Appl
32	14.2	52.6	41 2	US-08-909-768-4 Sequence 4, Appl
33	14.2	52.6	42 1	US-07-834-539A-17 Sequence 17, Appl
34	14.2	52.6	42 1	US-08-053-131-25 Sequence 25, Appl
35	14.2	52.6	42 1	US-08-645-641-25 Sequence 25, Appl
36	14.2	52.6	42 1	US-07-853-408B-25 Sequence 25, Appl
37	14.2	52.6	42 1	US-08-096-762-25 Sequence 25, Appl
38	14.2	52.6	42 2	US-08-800-353-17 Sequence 17, Appl
39	14.2	52.6	42 2	US-08-800-353-17 Sequence 17, Appl
40	14.2	52.6	42 4	US-08-758-417A-41 Sequence 193, App
41	14.2	52.6	42 4	US-08-758-417A-41 Sequence 193, App
42	14.2	52.6	42 4	US-08-758-417A-41 Sequence 193, App
43	14.2	52.6	42 5	PCT-US92-06185-15 Sequence 17, Appl
44	14.2	52.6	69 1	PCT-US92-10985-25 Sequence 25, Appl
45	14.2	52.6	69 1	US-08-434-001-122 Sequence 122, App

ALIGNMENTS

RESULT 1
US-08-152-621-7
Sequence 7, Application US/08152621
Patent No. 5652222
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: Selective inhibition of
TRUE OR INVENTION: Leukemic Cell Proliferation by ber-abl
TITLE OF INVENTION: Antisense Oligonucleotides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORNA
ADDRESS: 1800 Two Penn Center
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08152,621
FILING DATE: No. 5652222ember 15, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: No. 5652222e
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-152-621-7
Query Match 96.3%; Score 26; DB 1; Length 80;
Best Local Similarity 69.2%; Pred. No. 0.001;
Matches 18; Conservative 8; Mismatches 0; Gaps 0;

```
OY      1 UCUGACUUUUGAGCCUCAGGGUCUGAG   26
          :|:|||::|||::|||::|||::|||
DB     55 TCTGACTTTGAGCCTCAGGGTCTGAG   80
```

RESULT 2
US-08-30

Sequence 38, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZTD: 10102

COMPUTER READABLE FORM;

MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
 COMPUTER: IBM Ps/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/306,691B
 FILING DATE: September 15, 1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A.
 REGISTRATION NUMBER: 30,480
 REFERENCE/DOCKET NUMBER: 8321-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 TELEX: No. 57344039e
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 80 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

Query Match	96.3%	Score 26	DB 1	Length 80
Best Local Similarity	69.2%	Pred. No.	0.001	
Matches 18	Conservative 8	Mismatches 0	Indels 0	Gaps 0
QY	1 UCUGACUUUGAGCCGCCAGGUCUCAG	26		
Db	55 TCGACTTGTGAGCCCTCAGGGCTGTAG	80		

RESULT 3
PCT-US92-05035-7

```

? Sequence 7, Application PC/TUS9205035
?
? GENERAL INFORMATION:
?
? APPLICANT: Calabretta, Bruno
?
? APPLICANT: Gewirtz, Alan M.
?
? TITLE OF INVENTION: Selective Inhibition of
?
? TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-ab
?
? TITLE OF INVENTION: Antisense Oligonucleotides
?
? NUMBER OF SEQUENCES: 34
?
? CORRESPONDENCE ADDRESS:
?
? ADDRESSEE: Temple University - Of The Common-
?
? ADDRESSEE: wealth System of Higher Education

```

STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122

ZIP: 19122

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
3 COMPUTER: IBM PS/2
4 OPERATING SYSTEM: MS-DOS
5 SOFTWARE: Wordperfect 5.1
6
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: PCT/US92/05035
9 FILING DATE: 19920615
10 CLASSIFICATION: 514
11
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 07/718,302
14 FILING DATE: June 18, 1991
15
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 07/869,911
18 FILING DATE: April 14, 1991
19
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Monaco, Daniel A.
22 REGISTRATION NUMBER: 30,480
23 REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
24
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (215) 568-8383
27 TELEFAX: (215) 568-5549
28
29 TELEX: None
30
31 INFORMATION FOR SEQ. ID NO.: 7:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 80 Nucleotides
34 TYPE: NUCLEIC ACID
35 STRANDEDNESS: single stranded
36 TOPOLOGY: linear
37
38 PCT-US92-05035-7

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Query Match	96.38;	Score 26;	DB 5;	Length 80;
Best Local Similarity	69.28;	Pred. No. 0.001;		
Matches 18; Conservative	8;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 UCUGACUUUUGAGGCCUCAGGGGUCUGAG 26
          :|:||||::|||:|||:|||:|||
Db     55 TCTGACTTTGAGCCCTCAGGGTCTGAG 80
```

RESULT 4

US-08-013-419-1/c
Sequence 1, Application US/08013419
Patent No. 530635
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Product and Process for Isolating RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

STREET: Spring House Corporate Center, P.O. Box 457

CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/013,419
FILING DATE: 19930201
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UR1EFLUSA

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-013-419-1

Query Match 81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCGAGGUCUGA 25
Db 22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 5
US-08-122-795B-10/c
Sequence 10, Application US/08122795B
Patent No. 5635385
GENERAL INFORMATION:
APPLICANT: Lance H. Leopold
APPLICANT: Scott K. Shore
APPLICANT: Woole V. R. Reddy
APPLICANT: E. Premkumar Reddy
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna
ADDRESSEE: 6 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,795B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5635385e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-122-795B-10

Query Match 81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCGAGGUCUGA 25
Db 22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 6
US-08-525-818-1/c
Sequence 1, Application US/08525818
Patent No. 5728822
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and Methods
TITLE OF INVENTION: of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,818
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/113,727
FILING DATE:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIF1AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-940-9200
TELEFAX: 215-940-5618
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-525-818-1

Query Match 81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCGAGGUCUGA 25
Db 22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 7
US-09-028-184-1/c
Sequence 1, Application US/09028184
Patent No. 5985572
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and
TITLE OF INVENTION: Methods of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,184
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,818
FILING DATE: 07-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113,727
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: UIR1PUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-09-028-184-1

Query Match 81.5%; Score 22; DB 2; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCAGGUCUGA 25
||||:||||:||||:||||
Db 22 GACTTGAGCCTCAGGCTCGA 1

SUITE 8
T-US94-00680-1/c
Sequence 1, Application PC/TUS9400680
GENERAL INFORMATION:
APPLICANT: University of Iowa, Research Foundation
TITLE OF INVENTION: Quarternary Amine Surfactants and
TITLE OF INVENTION: Methods of using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00680
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113,727
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIR1APCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US94-00680-1

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCAGGUCUGA 25
||||:||||:||||:||||
Db 22 GACTTGAGCCTCAGGCTCGA 1

RESULT 9
PCT-US94-09963A-10/c
Sequence 10, Application PC/TUS9409963A
GENERAL INFORMATION:
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna
ADDRESS: 4 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09963A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
PCT-US94-09963A-10

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;


```

; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-872-678A-13

Query Match
Best Local Similarity 58.5%; Score 15.8; DB 1; Length 20;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 UUUGAGCCUCAGGUCUGA 25
Db 19 TTGAGCCTCAGACTGCA 1

RESULT 13
-08-170-095B-35
Sequence 35, Application US/08170095B
Patent No. 5563254
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Blood substitutes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,095B
FILING DATE: December 20, 1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5563254k, Henry P.
REGISTRATION/DOCKET NUMBER: 33200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown to applicant
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: beta globin sequence fragment
HYPOTHETICAL: no
US-08-170-095B-35

Query Match
Best Local Similarity 57.8%; Score 15.6; DB 1; Length 67;
Matches 13; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 UGACUUGAGCCUCAGGUCUGA 26
Db 44 TGCTAGSAGCCTGAGGTCTGAG 67

RESULT 14
US-08-921-887-48
Sequence 48, Application US/08921887
Patent No. 6030771

; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE: Hepatitis virus
US-08-921-887-48

Query Match
Best Local Similarity 57.8%; Score 15.6; DB 3; Length 80;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 CUGACUUGAGCCUCAGGUCU 23
Db 59 CTGAGTCTGAGCCTCAGGTGT 80

RESULT 15
US-08-761-131-7/c
Sequence 7, Application US/08761131
Patent No. 5804384
GENERAL INFORMATION:
APPLICANT: M Iler, Uwe R. et al.
TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vysis, Inc.
STREET: 3100 Woodcreek Drive
CITY: Downers Grove
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60515
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
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Mon Dec 23 08:48:00 2002

us-09-121-239-23.rni

Page 7

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/761,131
3 FILING DATE:
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER:
7 FILING DATE:
8 ATTORNEY/AGENT INFORMATION:
9 NAME: Galloway, No. 5804384val B.
10 REGISTRATION NUMBER: 33,595
11 REFERENCE/DOCKET NUMBER: 01886/064001
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 708-271-7417
14 TELEFAX: 708-271-7048
15 TELEX: 200154
16 INFORMATION FOR SEQ. ID NO: 7:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 20 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: single
21 TOPOLOGY: linear
22 MOLECULE TYPE: Genomic DNA
23
24
25
26
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 (Search time 15.502 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-26
Perfect score: 18
Sequence: 1 GAATTCATCGAGCATGC 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- 1: /cgn2_6/ptodata/1/lna/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/lna/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/lna/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/lna/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/lna/PCU03.COMB.seq.*
- 6: /cgn2_6/ptodata/1/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	13.8	76.7	37	1	US-08-444-231-3
2	13.8	76.7	37	1	US-08-152-443A-3
3	13.8	76.7	73	4	US-09-625-188-36
4	12.8	71.1	20	1	US-08-480-552-13
5	12.8	71.1	20	1	US-08-204-740-1
6	12.8	71.1	20	2	US-08-486-382-1
7	12.8	71.1	20	2	US-08-485-657A-1
8	12.8	71.1	20	2	US-08-258-371-22
9	12.8	71.1	20	3	US-09-235-546-13
10	12.8	71.1	20	3	US-08-923-208-13
11	12.8	71.1	20	3	US-09-081-167A-1
12	12.8	71.1	20	3	US-09-081-395-1
13	12.8	71.1	20	3	US-08-751-230-22
14	12.8	71.1	20	3	US-08-499-082-22
15	12.8	71.1	20	4	US-09-416-833-1
16	12.8	71.1	20	4	US-09-258-372-22
17	12.8	71.1	20	5	PCY-US95-02303-1
18	12.8	71.1	20	5	PCY-US95-02303-1
19	12.8	71.1	23	1	US-08-480-552-14
20	12.8	71.1	23	1	US-08-204-740-2
21	12.8	71.1	23	2	US-08-486-382-2
22	12.8	71.1	23	2	US-08-485-657A-2
23	12.8	71.1	23	2	US-09-258-371-23
24	12.8	71.1	23	3	US-09-235-546-2
25	12.8	71.1	23	3	US-08-923-208-14
26	12.8	71.1	23	3	US-09-081-167A-2
27	12.8	71.1	23	3	US-09-081-167A-2

c 28	12.8	71.1	23	3	US-09-081-395-2	Sequence 2, Appl
c 29	12.8	71.1	23	3	US-08-751-230-23	Sequence 23, Appl
c 30	12.8	71.1	23	3	US-09-499-082-23	Sequence 23, Appl
c 31	12.8	71.1	23	4	US-09-416-833-2	Sequence 2, Appl
c 32	12.8	71.1	23	4	US-09-258-372-23	Sequence 2, Appl
c 33	12.8	71.1	23	4	US-09-568-315-14	Sequence 14, Appl
c 34	12.8	71.1	23	5	PCY-US95-02303-2	Sequence 2, Appl
c 35	12.8	71.1	23	5	PCY-US95-02303-2	Sequence 2, Appl
c 36	12.8	67.8	24	4	US-09-593-012-214	Sequence 214, App
c 37	12.2	67.8	36	2	US-08-864-224-3	Sequence 16, Appl
c 38	12.2	67.8	37	4	US-08-900-574-16	Sequence 3, Appl
c 39	12	66.7	39	3	US-09-428-589-3	Sequence 21, Appl
c 40	11.8	65.6	20	3	US-09-121-920-21	Sequence 61, Appl
c 41	11.8	65.6	21	4	US-09-423-233-61	Sequence 3, Appl
c 42	11.8	65.6	24	4	US-09-556-668-3	Sequence 61, Appl
c 43	11.8	65.6	29	3	US-08-258-287B-62	Sequence 62, Appl
c 44	11.8	65.6	29	3	US-08-368-704C-60	Sequence 60, Appl
c 45	11.8	65.6	37	4	US-08-900-574-15	Sequence 15, Appl

ALIGNMENTS

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RESULT 1
US-08-444-231-3
; Sequence 3, Application US/08444231
; Patent No. 5652210
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,231
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/152,443
; FILING DATE: 15-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-444-231-3
Query Match      76.7%; Score 13.8; DB 1; Length 37;
Best Local Similarity 88.2%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 GGAATCATCGAGCATG 17
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Db 14 GGAATCATCAAGCATG 30

RESULT 2
US-08-152-443A-3
; Sequence 3, Application US/08152443A
; Patent No. 5663070

GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-152-443A-3

Query Match 76.7%; Score 13.8; DB 1; Length 37;

Best Local Similarity 88.2%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
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Db 14 GGAATCATCAAGCATG 30

RESULT 3
US-09-625-188-36
; Sequence 36, Application US/09625188
; Patent No. 6307037

GENERAL INFORMATION:

APPLICANT: No. 6307037artis AG
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/5-31285P1
CURRENT APPLICATION NUMBER: US/09/625,188
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 73
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-625-188-36

Query Match 76.7%; Score 13.8; DB 4; Length 73;
Best Local Similarity 88.2%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
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Db 44 GGAATCATCAAGCATG 60

RESULT 4
US-08-480-552-13
; Sequence 13, Application US/08480552
; Patent No. 5665550

GENERAL INFORMATION:

APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Genes And Genetic Elements Associated
TITLE OF INVENTION: With Sensitivity To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,552
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/033,086
FILING DATE: 09 MAR 1993
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 93,354
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/345-9110
TELEFAX: 617/345-9111

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-480-552-13

Query Match 71.1%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCATG 18
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Db 1 AATCATCATGATG 16

RESULT 5
US-08-204-740-1
; Sequence 1, Application US/08204740

Patent No. 5753432
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Kazarov, Alexander
APPLICANT: Mazo, Ilya
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods for identifying Genetic
TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allgretti & Witcoff, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5753432nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-204-740-1
Query Match 71.1%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 3 AATCATCGAGCATGG 18
DB 1 AATCATCGAGCATGG 16
RESULT 6
US-08-486-382-1
Sequence 1, Application US/08486382
Patent No. 5866327
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Association of Kinesin with Sensitivity
TITLE OF INVENTION: To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,382
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,571
FILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5866327nan, Kevin E.
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-382-1
Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 3 AATCATCGAGCATGG 18
DB 1 AATCATCGAGCATGG 16
RESULT 7
US-08-485-657A-1
Sequence 1, Application US/08485657A
Patent No. 5942389
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-485-657A-1

Query Match
Best Local Similarity 71.1%; Score 12.8; DB 2; Length 20;
Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCGATGG 18
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Db 1 AATCATCGATGATGG 16

RESULT 8
US-09-258-371-22
; Sequence 22, Application US/09258371
; Patent No. 5986078

GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Rikbovsk, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
NUMBER OF SEQUENCES: 23
TITLE OF INVENTION: SUPPRESSOR GENE INGI

CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA

COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371

FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/751,230

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mool, Leslie A.
REGISTRATION NUMBER: 37,047

REFERENCE/DOCKET NUMBER: 028722-144

TELEPHONE: 415-854-7400

TELEFAX: 415-854-8275

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-09-258-371-22

Query Match
Best Local Similarity 71.1%; Score 12.8; DB 2; Length 20;
Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCGATGG 18
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Db 1 AATCATCGATGATGG 16

RESULT 9
US-09-235-546-1
; Sequence 1, Application US/09235546
; Patent No. 6043340

GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Association of Kinesin with Sensitivity
TITLE OF INVENTION: To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,546

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,382

FILING DATE:

APPLICATION NUMBER: US 08/177,571

FILING DATE: 05 JAN 1994

ATTORNEY/AGENT INFORMATION:

NAME: No. 6043340nan, Kevin E.
REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-A

TELEPHONE: 312/715-1000

TELEFAX: 312/715-1234

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-235-546-1

Query Match
Best Local Similarity 71.1%; Score 12.8; DB 3; Length 20;
Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCGATGG 18
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Db 1 AATCATCGATGATGG 16

RESULT 10
US-08-929-208-13
; Sequence 13, Application US/08929208
; Patent No. 6060244

GENERAL INFORMATION:

APPLICANT: Gudkov, Andrei

APPLICANT: Roninson, Igor B.

TITLE OF INVENTION: Genes And Genetic Elements Associated

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,208
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/480,552
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A. 33,923
REGISTRATION NUMBER: 93,354
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/345-9100
TELEFAX: 617/345-9111
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-929-208-13

Query Match      71.1%  Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 AATCATCGAGCATGG 18
DB      1 AATCATCGATGATGG 16

RESULT 11
US-09-081-167A-1
Sequence 1, Application US/09081167A
Patent No. 6083745
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Kazarov, Alexander
APPLICANT: Mazo, Ilya
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods for Identifying Genetic
TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
TITLE OF INVENTION: Growth in Cancer Cells
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,167A
FILING DATE: 18-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083745nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-KK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-081-167A-1

Query Match      71.1%  Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 AATCATCGAGCATGG 18
DB      1 AATCATCGATGATGG 16

RESULT 12
US-09-081-395-1
Sequence 1, Application US/09081395
Patent No. 6083746
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Kazarov, Alexander
APPLICANT: Mazo, Ilya
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods for Identifying Genetic
TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
TITLE OF INVENTION: Growth in Cancer Cells
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,395
FILING DATE: 18-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083746nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-KK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-081-395-1

Query Match      71.1%  Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 AATCATCGAGCATGG 18
DB      1 AATCATCGATGATGG 16
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RESULT 13
US-08-751-230-22
; Sequence 22, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Radoowl, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,230
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-751-230-22

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCATGG 18
||||||| | |||
Db 1 AATCATCGATGATGG 16

RESULT 14
US-09-499-082-22
; Sequence 22, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Radoowl, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/499,082
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,158
; FILING DATE: 27-MAR-1997
; APPLICATION NUMBER: US 08/751230
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-854-7400
; TELEFAX: 650-854-8275
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-499-082-22

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCATGG 18
||||||| | |||
Db 1 AATCATCGATGATGG 16

RESULT 15
US-09-416-833-1
; Sequence 1, Application US/09416833
; Patent No. 6197521
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allgretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,740

Mon Dec 23 08:48:01 2002

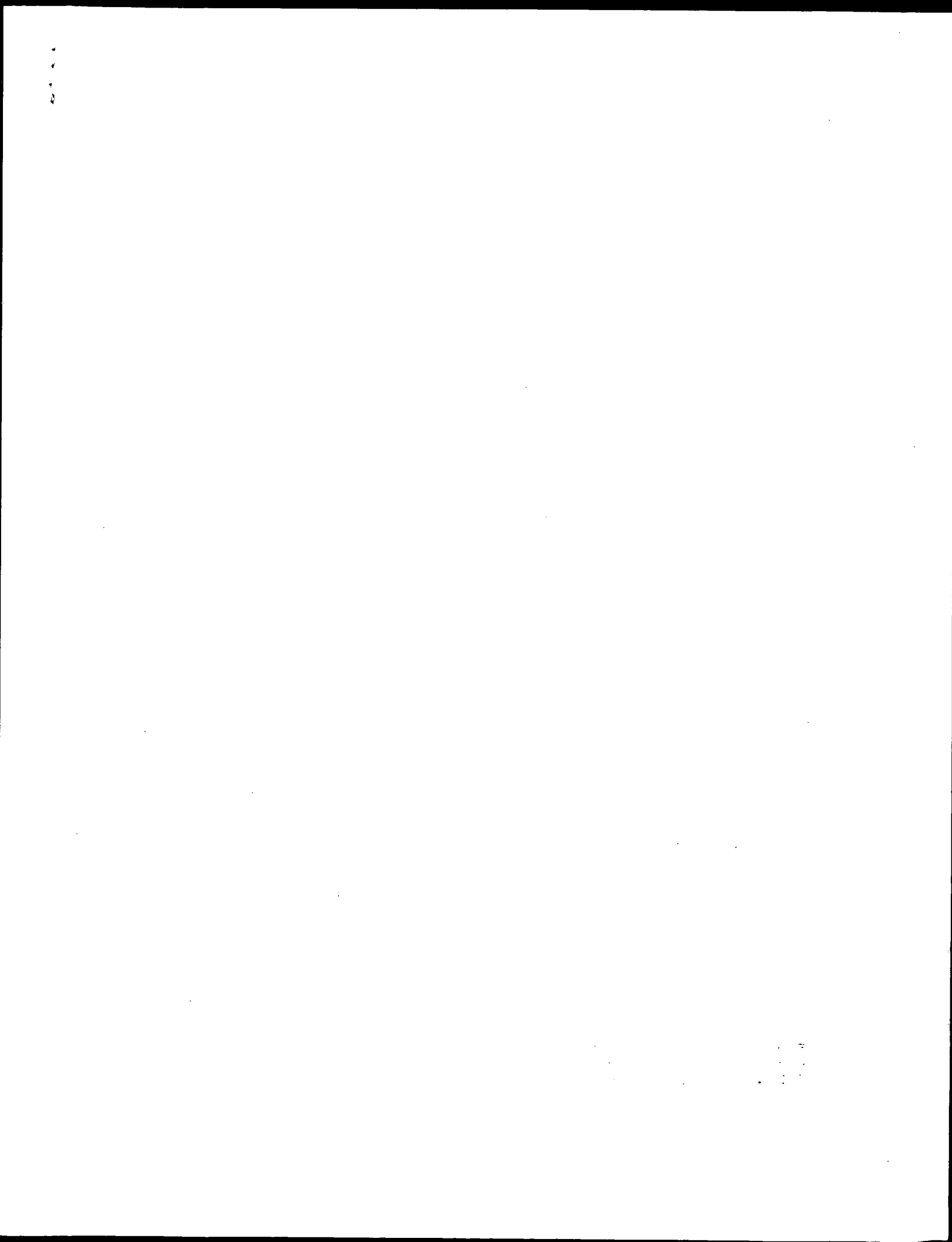
us-09-121-239-26.rni

Page 7

FILED DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6197521nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-416-833-1

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 AATCATCGAGCATGG 18
||||||| |
Db 1 AATCATCGAGCATGG 16

Search completed: December 21, 2002, 11:58:26
Job time : 16.502 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 : Search time 22.3918 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-27
Perfect score: 26
Sequence: 1 CACTGAGCCACTGGATTAAAGCAGAG 26

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/pdata/1/ina/5A.COMB.seq:*
2: /cgn2_6/pdata/1/ina/5B.COMB.seq:*
3: /cgn2_6/pdata/1/ina/5A.COMB.seq:*
4: /cgn2_6/pdata/1/ina/5B.COMB.seq:*
5: /cgn2_6/pdata/1/ina/PCMTUS.COMB.seq:*
6: /cgn2_6/pdata/1/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	56	1	US-07-940-652-16
2	26	100.0	56	1	US-08-255-553-16
3	26	100.0	90	5	PCT-US93-06251-14
4	25	96.2	40	4	US-09-358-972-125
5	25	96.2	41	4	US-09-358-972-126
6	25	96.2	66	1	US-07-940-652-13
7	25	96.2	66	1	US-08-255-553-13
8	21.4	82.3	40	1	US-08-761-131-2
9	18	69.2	18	1	US-08-761-131-4
10	16	61.5	88	4	US-09-171-759-17
11	15	57.7	22	4	US-09-358-972-127
12	15	57.7	22	4	US-09-358-972-128
13	15	57.7	22	4	US-09-406-064-97
14	15	57.7	22	4	US-09-406-064-98
15	15	57.7	22	4	US-08-761-131-5
16	15	57.7	22	4	US-08-761-131-2
17	14.4	55.4	28	1	US-08-479-852-12
18	14.4	55.4	28	1	US-08-479-852-14
19	14.4	55.4	28	1	US-08-479-852-98
20	14.4	55.4	28	1	US-08-479-852-92
21	14.4	55.4	28	2	US-08-462-646-12
22	14.4	55.4	28	2	US-08-462-646-64
23	14.4	55.4	28	2	US-08-462-646-12
24	14.4	55.4	28	2	US-08-462-646-92
25	14.4	55.4	28	2	US-09-013-406-12
26	14.4	55.4	28	4	US-09-013-406-14
27	14.4	55.4	28	4	US-09-013-406-78

28	14.4	55.4	28	4	US-09-013-406-92	Sequence 92, Appl
29	14.4	55.4	30	1	US-08-171-389-486	Sequence 486, App
30	14.4	55.4	30	1	US-08-171-389-487	Sequence 487, App
31	14.4	55.4	50	1	US-08-123-936-486	Sequence 486, App
32	14.4	55.4	50	1	US-08-123-936-487	Sequence 487, App
33	14.4	55.4	50	2	US-08-475-228A-486	Sequence 486, App
34	14.4	55.4	50	2	US-08-475-228A-487	Sequence 487, App
35	14.4	55.4	50	3	US-08-482-080A-486	Sequence 486, App
36	14.4	55.4	50	3	US-08-482-080A-487	Sequence 487, App
37	14.4	55.4	50	4	US-09-354-947-486	Sequence 486, App
38	14.4	55.4	50	4	US-09-354-947-487	Sequence 487, App
39	14.4	55.4	50	5	PCT-US93-12388-486	Sequence 486, App
40	14.4	55.4	50	5	PCT-US93-12388-487	Sequence 487, App
41	14.4	53.8	37	1	US-08-343-682-12	Sequence 12, Appl
42	14.4	53.8	47	4	US-09-641-638-1213	Sequence 1213, Appl
43	14.4	53.8	49	1	US-08-343-682-11	Sequence 11, Appl
44	13.6	51.5	20	1	US-08-259-745A-46	Sequence 46, Appl
45	13.4	51.5	24	2	US-08-474-450A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-940-652-16
Sequence 16, Application US-07-940652
Patent No. 542413
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-07-940,652
FILING DATE: 19920904
CLASSIFICATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-07-827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-940-652-16
Query Match 100.0%: Score 26; DB 1; Length 56;
Best Local Similarity 100.0%: Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACTGAGCCACTGGATTAAAGCAGAG 26
DB 10 CACTGAGCCACTGGATTAAAGCAGAG 35

RESULT 2
US-08-255-553-16
Sequence 16, Application US/0825553
Patent No. 5451503
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-255-553-16

Query Match 100.0%; Score 26; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGATTTAAGCAGAG 26
DB 10 CACTGAGCCACTGATTTAAGCAGAG 35

RESULT 3
PCT-US93-06251-4
Sequence 4, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivial Synthesis of Oligonucleotides Containing
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-4

Query Match 100.0%; Score 26; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGATTTAAGCAGAG 26
DB 45 CACTGAGCCACTGATTTAAGCAGAG 70

RESULT 4
US-09-358-972-125/C
Sequence 125, Application US/09358972
Patent No. 6235480
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/358,972
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 125
LENGTH: 40
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: native bcr
US-09-358-972-125

Query Match 96.2%; Score 25; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTGAGCCACTGATTTAAGCAGAG 26

Db 40 ACTCAGCCACTGATTTAAGCAG 16
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RESULT 5
US-09-358-972-126/c
Sequence 126, Application US/09358972
Patent No. 6235480
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/358,972
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 126
LENGTH: 41
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: bcr/abl translocation
US-09-358-972-126
Query Match 96.2%; Score 25; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 ACTCAGCCACTGATTTAAGCAG 26
|||||
Db 41 ACTCAGCCACTGATTTAAGCAG 17
RESULT 6
US-07-940-652-13/c
Sequence 13, Application US/07940652
Patent No. 542413
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 19920904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 66
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-940-652-13
Query Match 96.2%; Score 25; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 ACTCAGCCACTGATTTAAGCAG 26
|||||
Db 66 ACTCAGCCACTGATTTAAGCAG 42
RESULT 7
US-08-255-553-13/c
Sequence 13, Application US/08255553
Patent No. 5451503
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 66
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-255-553-13
Query Match 96.2%; Score 25; DB 1; Length 66;

Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ACTCAGCCACTGATTTAAGCAG 26
|||||
DB 66 ACTCAGCCACTGATTTAAGCAG 42

RESULT 8

US-08-761-131-2
; Sequence 2, Application US/08761131
; Patent No. 5804384
; GENERAL INFORMATION:
; APPLICANT: M Iler, Uwe R. et al.
; TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
; TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vysis, Inc.
; STREET: 3100 Woodcreek Drive
; CITY: Downers Grove
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60515
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761.131
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5804384val B.
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: 01886/064001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-271-7417
; TELEFAX: 708-271-7048
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-761-131-2

Query Match 82.3%; Score 21.4; DB 1; Length 40;
Best Local Similarity 95.7%; Pred. No. 0.034; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCAGCCACTGATTTAAGCAG 24
|||||
DB 1 ACTCAGCCACTGATTTAAGTAG 23

RESULT 9

US-08-761-131-4/c
; Sequence 4, Application US/08761131
; Patent No. 5804384
; GENERAL INFORMATION:
; APPLICANT: M Iler, Uwe R. et al.
; TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
; TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vysis, Inc.

STREET: 3100 Woodcreek Drive
CITY: Downers Grove
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60515
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761.131
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5804384val B.
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: 01886/064001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-271-7417
TELEFAX: 708-271-7048
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-761-131-4

Query Match 69.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTCAGCCACTGATTTA 19
|||||
DB 18 ACTCAGCCACTGATTTA 1

RESULT 10

US-09-171-759-17
; Sequence 17, Application US/09171759
; Patent No. 6346415
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew
; TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
; AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMB
; AAV VECTORS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171.759
; FILING DATE: 20-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

NAME: Dylan, Tyler M
 REGISTRATION NUMBER: 37,612
 REFERENCE/DOCKET NUMBER: 22627-20038.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 88 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-171-759-17

Query Match 61.5% Score 16; DB 4; Length 88;
 Best Local Similarity 79.2% Pred. No. 26;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTCAGCCACTGATTAAGCAGAG 26
 DB 43 CCCACCCCGTATATTAAGCAGAG 66

RESULT 11
 US-09-171-759-18/c
 Sequence 18, Application US/09171759
 Patent No. 6346415
 GENERAL INFORMATION:
 APPLICANT: Feldhaus, Andrew
 TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
 AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMBINANT
 AAV VECTORS
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESSES:
 ADDRESS: MORRISON & ROEBSTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/171,759
 FILING DATE: 20-Oct-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Dylan, Tyler M
 REGISTRATION NUMBER: 37,612
 REFERENCE/DOCKET NUMBER: 22627-20038.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 88 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-171-759-18

Query Match 61.5% Score 16; DB 4; Length 88;
 Best Local Similarity 79.2% Pred. No. 26;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CTCAGCCACTGATTAAGCAGAG 26
 DB 50 CCCACCCCGTATATTAAGCAGAG 27

RESULT 12
 US-09-358-972-127
 Sequence 127, Application US/09358972
 Patent No. 6235480
 GENERAL INFORMATION:
 APPLICANT: Shultz, John W.
 APPLICANT: Lewis, Martin K.
 APPLICANT: Lieppe, Donna
 APPLICANT: Mandrekar, Michelle
 APPLICANT: Kephart, Daniel
 APPLICANT: Rhodes, Richard B.
 APPLICANT: Andrews, Christine A.
 APPLICANT: Hartnett, James R.
 APPLICANT: Gu, Trent
 APPLICANT: Olson, Ryan J.
 APPLICANT: Wood, Keith W.
 APPLICANT: Welch, Roy
 TITLE OF INVENTION: Nucleic Acid Detection
 FILE REFERENCE: Pro-103 6868/75528
 CURRENT APPLICATION NUMBER: US/09/358,972
 CURRENT FILING DATE: 1999-07-22
 EARLIER APPLICATION NUMBER: 09/252,436
 EARLIER FILING DATE: 1999-02-18
 EARLIER APPLICATION NUMBER: 09/042,287
 EARLIER FILING DATE: 1998-03-13
 NUMBER OF SEQ ID NOS: 290
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 127
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: probe for native bcr
 US-09-358-972-127

Query Match 57.7% Score 15; DB 4; Length 22;
 Best Local Similarity 100.0% Pred. No. 59;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 TCGATTTAAGCAGAG 26
 DB 1 TCGATTTAAGCAGAG 15

RESULT 13
 US-09-358-972-128
 Sequence 128, Application US/09358972
 Patent No. 6235480
 GENERAL INFORMATION:
 APPLICANT: Shultz, John W.
 APPLICANT: Lewis, Martin K.
 APPLICANT: Lieppe, Donna
 APPLICANT: Mandrekar, Michelle
 APPLICANT: Kephart, Daniel
 APPLICANT: Rhodes, Richard B.
 APPLICANT: Andrews, Christine A.
 APPLICANT: Hartnett, James R.
 APPLICANT: Gu, Trent
 APPLICANT: Olson, Ryan J.
 APPLICANT: Wood, Keith W.
 APPLICANT: Welch, Roy
 TITLE OF INVENTION: Nucleic Acid Detection
 FILE REFERENCE: Pro-103 6868/75528
 CURRENT APPLICATION NUMBER: US/09/358,972
 CURRENT FILING DATE: 1999-07-22
 EARLIER APPLICATION NUMBER: 09/252,436

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; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 128
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: probe for bcr/abl translocation
US-09-358-972-128

Query Match
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGATTTAAGCAGAG 26
      |||||
DB 1 TGGATTTAAGCAGAG 15

RESULT 14
US-09-406-064-97
; Sequence 97, Application US/09406064
; Patent No. 6270973
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/406,064
; EARLIER FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 97
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-406-064-97

Query Match
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGATTTAAGCAGAG 26
      |||||
DB 1 TGGATTTAAGCAGAG 15

RESULT 15
US-09-406-064-98
; Sequence 98, Application US/09406064
; Patent No. 6270973
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
```

```

; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/406,064
; EARLIER FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 98
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-406-064-98

Query Match
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGATTTAAGCAGAG 26
      |||||
DB 1 TGGATTTAAGCAGAG 15
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Search completed: December 21, 2002, 11:58:27
Job time : 23.3918 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 1664.08 Seconds
(without alignments)
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Title: US-09-121-239-1

Perfect score: 54
Sequence: 1 TAAATTAATACGACTCACTA.....CCCTGAGCCTCAAGTCAGA 54

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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25: em_gss_other:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	23.4	43.3	79	9	AJ282930	4A3A-PIE1
2	23.2	43.0	75	9	AJ282930	4A3A-PIE1
3	23	42.6	70	17	AQ797214	RPCI-22-4
4	23	42.6	69	17	BH217910	1006061D0
5	22.6	41.9	100	9	AI353756	zeh0940.s
6	22.4	41.5	46	9	AI096189	SWAMCACC26

C	7	22.4	41.5	50	10	AM160061
C	8	22.4	41.5	50	10	AM172194
C	9	22.4	41.5	53	10	AM160055
C	10	22.4	41.5	59	10	AM041922
C	11	22.4	41.5	60	10	AM172242
C	12	22.4	41.5	62	9	AI096287
C	13	22.4	41.5	62	10	AM159998
C	14	22.4	41.5	64	10	AM159945
C	15	22.4	41.5	66	10	AM172179
C	16	22.4	41.5	68	9	AI218795
C	17	22.4	41.5	69	9	AI096196
C	18	22.4	41.5	70	9	AA273106
C	19	22.4	41.5	73	9	AA680645
C	20	22.4	41.5	74	10	AM159913
C	21	22.4	41.5	75	10	AM160023
C	22	22.4	41.5	75	10	AM160023
C	23	22.4	41.5	76	10	AM160031
C	24	22.4	41.5	76	10	AM160031
C	25	22.4	41.5	80	9	AA681006
C	26	22.4	41.5	80	9	AJ494595
C	27	22.4	41.5	91	9	AI066878
C	28	22.4	41.5	93	10	AM203873
C	29	22.4	41.5	95	10	AM172121
C	30	22.4	41.5	95	10	AM172121
C	31	22.4	41.5	97	14	R293479
C	32	22.4	41.5	97	9	AA051907
C	33	22.4	41.5	97	9	AI058116
C	34	22.4	41.5	98	10	AM041925
C	35	22.4	41.5	98	10	AM160064
C	36	22.4	41.5	100	9	AI239372
C	37	22.2	41.1	100	13	BM027537
C	38	21.8	40.4	89	14	N28043
C	39	21.8	40.4	91	14	R29262
C	40	21.8	40.4	92	14	N28040
C	41	21.8	40.4	95	9	AI353162
C	42	21.8	40.4	95	9	AI353583
C	43	21.8	40.4	96	9	AI616894
C	44	21.8	40.4	96	9	AI617314
C	45	21.8	40.4	96	10	AM455598

ALIGNMENTS

RESULT 1	AJ282930	79 bp	mRNA	linear	EST 30-JUN-2000
LOCUS	AJ282930	4A3A-PIE1-R	Anopheles gambiae	immune competent	4A3A Anopheles
DEFINITION	AJ282930	gambiae cDNA clone 4A3A-PIE1, mRNA sequence.			
ACCESSION	AJ282930				
VERSION	AJ282930.1	GI:6930809			
KEYWORDS	EST.				
SOURCE	AFRICAN malaria mosquito.				
ORGANISM	Anopheles gambiae				
REFERENCE	1 (bases 1 to 79)				
AUTHORS	Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansong, W., Soares, M.B. and Kafatos, F.C.				
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.				
MEDLINE	20300950				
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos Laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany. Location/Qualifiers 1..79 /organism="Anopheles gambiae"				
FEATURES	source				

/strain="4A r/r"
 /db_xref="taxon:7165"
 /clone_lib="Anopheles gambiae immune competent 4A3A"
 /cell_line="Immune competent 4A3A"
 /lab_host="E. coli DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

BASE COUNT

26 a 16 c 18 g 18 t 1 others

Query Match 43.3%; Score 23.4; DB 9; Length 79;
 Best Local Similarity 96.0%; Pred. No. 1.2e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AATTATATACGACTCATATAGGGA 26
 ||||||||||||||||||||
 Db 28 AATTATATACGACTCATATAGGGA 52

RESULT 2

LOCUS A1087772/c 75 bp mRNA linear EST 18-ANG-1998
 DEFINITION SMOVAMCA02F02SK Onchocerca volvulus adult male cDNA (SAM98MLW-OVAM)

ACCESSION A1087772
 VERSION A1087772.1 GI:3426748
 KEYWORDS EST.
 SOURCE Onchocerca volvulus.
 ORGANISM Onchocerca volvulus.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.

REFERENCE

1 (bases 1 to 75)

AUTHORS Lizotte-Waniewski, M. and Williams, S.A.
 TITLE Genes expressed in adult male stage of *Onchocerca volvulus*
 JOURNAL Unpublished (1998)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences
 Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genomesmith.edu
 Seq primer: pbuescript SK.

FEATURES

Location/Qualifiers

1..75

/organism="Onchocerca volvulus"

/db_xref="taxon:6282"

/clone="SMOVAMCA02F02"

/clone_lib="Onchocerca volvulus adult male cDNA (SAM98MLW-OVAM)"

/sex="male"

/dev_stage="adult"

/lab_host="XLI-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans; six adult male worms of *Onchocerca volvulus* were isolated from consenting patients and quick frozen. Adult male mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2 x 10⁵ independent recombinants and the average insert size is ~1100bp. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genomesmith.edu."

BASE COUNT

13 a 19 c 24 g 19 t

ORIGIN

Query Match 43.0%; Score 23.2; DB 9; Length 75;
 Best Local Similarity 70.5%; Pred. No. 1.4e+02;
 Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 2 AATTATATACGACTCATATAGGGAAGACTGACCGTGGGCTC 45
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 Db 67 AATTATATACGACTCATATAGGGAAGACTGACCGTGGGCTC 24

RESULT 3

LOCUS A0797214/c 30 bp DNA linear GSS 26-JAN-2001
 DEFINITION RPCI-22-458D11-T7 RPCI-22 Mouse (129S6/SvEvTac) genomic library Mus

ACCESSION A0797214
 VERSION A0797214
 KEYWORDS GSS.

SOURCE

house mouse.
Mus musculus

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Osoegawa, K., Tateo, M., Woon, P. Y., Frengen, E., Mammoser, A. G., Catalanese, J. J., Hayashizaki, Y., and de Jong, P. J.
 TITLE Bacterial artificial chromosome libraries for mouse sequencing and functional analysis
 JOURNAL Genome Res. 10 (1), 116-128 (2000)
 MEDLINE 20113121
 COMMENT Contact: de Jong, P. J.
 Children's Hospital Oakland Research Institute
 747 Fifty Second Street, Oakland, CA 94609-1809, USA
 Tel: 510 450 7911
 Fax: 510 450 7924
 Email: pdejong@mail.cho.org
 BAC end sequences. For clone availability please contact Pieter de Jong (pdejong@mail.cho.org). BACPAC Resources WWW site: www.choil.org/bacpac
 Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers

1..30

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RPCI-22-458D11-T7"

/clone_lib="RPCI-22 Mouse (129S6/SvEvTac) genomic library"

/sex="Female"

/cell_type="Spleen"

/note="Vector: pBAC3.6; BAC clones in E. coli DH10B"

BASE COUNT

6 a 8 c 7 g 9 t

Query Match 42.6%; Score 23; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 TAATACGACTCATATAGGAGA 28
 ||||||||||||||||||||
 Db 24 TAATACGACTCATATAGGAGA 2

RESULT 4

LOCUS BH217910 69 bp DNA linear GSS 08-NOV-2001
 DEFINITION 1006061D02.2EL_x1 1006 - Rescueu Gtid G zea mays genomic, DNA

ACCESSION BH217910
 VERSION BH217910.1 GI:16810050
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogonaceae; Zea.
1 (bases 1 to 69)
Walbot, V.
Maize genomic sequences found using engineered Rescemu transposon
Unpublished (2001)
Contact: Walbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006061 row: 21
Class: transposon-tagged.
Location/Qualifiers

FEATURES

source

1..69
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone.lib="1006 - Rescemu Grid G"
/issue.type="leaf"
/dev.stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescemu (engineered from
pBluescript backbone); Site.1: BamHI; Site.2: BglII;
Rescemu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescemu, go to the web
site 'www.zmdd.lafate.edu' and follow the links for
'Rescemu'. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT 16 a 18 c 21 g 14 t
ORIGIN

Query Match 42.6%; Score 23; DB 17; Length 69;
Best Local Similarity 83.9%; Pred. No. 1.5e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 TAAATGACGACTACTATAGGAGGAGGAGC 36
|||||
DB 2 TAAATGACGACTACTATAGGAGGAGGAGC 32

RESULT 5
AL353756/c 100 bp mRNA linear EST 04-JAN-1999
LOCUS zeh0940.seq.F zebrafish Embryonic Heart cDNA Library Danio rerio
DEFINITION cDNA 5', mRNA sequence.
ACCESSION AL353756
VERSION AL353756.1 GI:4093909
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 100)
Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and Liew
C.C.
Identification and Characterization of Expressed Sequence Tags from
an Embryonic Zebrafish Heart cDNA Library
Unpublished (1999)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School

75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: clevelandics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAAGCTCGAATTAACCCCTCACTAAGG 3'
BACKWARD: 5' CCAGTGAATGATATAGCGACTACTATAGGCG 3'
Seq primer: 5' GAAATTAACCCCTCACTAAGG 3'.
Location/Qualifiers

FEATURES

source

1..100
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone.lib="zebrafish Embryonic Heart cDNA Library"
/dev.stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue MRF"
/note="Organ: heart; Vector: Lambda ZAP Express; Site.1:
EcoRI; Site.2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."

BASE COUNT 20 a 27 c 27 g 26 t
ORIGIN

Query Match 41.9%; Score 22.6; DB 9; Length 100;
Best Local Similarity 86.2%; Pred. No. 2.7e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AATTAATGACGACTACTATAGGAGGAGC 30
|||||
DB 98 AATTAATGACGACTACTATAGGAGGAGC 70

RESULT 6
AT096189/c 46 bp mRNA linear EST 19-AUG-1998
LOCUS SNAMCNC26D04SK Brugia malayi adult male cDNA (SNM94NL-BmAM) Brugia
DEFINITION malayi cDNA clone SNAMCNC26D04 5', mRNA sequence.
ACCESSION AT096189
VERSION AT096189.1 GI:3445100
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 46)
Williams, S.A.
Genes expressed in adult males of Brugia malayi
Unpublished (1995)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers

FEATURES

source

1..46
/organism="Brugia malayi"
/strain="FRS labs"
/db_xref="taxon:6279"
/clone.lib="SNAMCNC26D04"
/clone.lib="Brugia malayi adult male cDNA (SNM94NL-BmAM)"
/note="Vector: lambda UniZap XR; Site.1: EcoR I; Site.2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from adult males of Brugia malayi
isolated from jirds and converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
Rnase H and DNase I. The library had 4.6 x 10⁶

independent recombinants and average insert size was 800 base pairs. The library was constructed by Noelle Ling. The library is available from Dr. S.A. Williams, email genome@smith.edu."

BASE COUNT

9 a 12 c 15 g 10 t

Query Match 41.5%; Score 22.4; DB 9; Length 46;
Best local similarity 72.5%; Pred. No. 2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACTCAGACCTGAGGCTC 45
|||||
DB 44 TAATACGACTCACTATAGGCGCAATGGGTACCGGCCCC 5

RESULT 7

AM160061/c 50 bp mRNA linear EST 05-NOV-1999
LOCUS SW14CAK0601SK Brugia malayi L4 cDNA (SAM99MLM-Bml4) Brugia malayi
DEFINITION CDNA clone SW14CAK0601 5', mRNA sequence.
ACCESSION AM160061
VERSION AM160061.1 GI:6272090
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.

REFERENCE 1 (bases 1 to 50)
AUTHORS Williams, S.A.
TITLE Genes expressed in fourth stage larvae of Brugia malayi
JOURNAL Unpublished (1999)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pbluescript SK.
Location/Qualifiers
1..50

FEATURES
source

BASE COUNT
ORIGIN
Query Match 41.5%; Score 22.4; DB 10; Length 50;
Best local similarity 72.5%; Pred. No. 2.1e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACTCAGACCTGAGGCTC 45
|||||
DB 44 TAATACGACTCACTATAGGCGCAATGGGTACCGGCCCC 5

BASE COUNT
ORIGIN
Query Match 41.5%; Score 22.4; DB 10; Length 50;
Best local similarity 72.5%; Pred. No. 2.1e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACTCAGACCTGAGGCTC 45
|||||
DB 44 TAATACGACTCACTATAGGCGCAATGGGTACCGGCCCC 5

RESULT 8
AM172194/c

LOCUS AM172194 50 bp mRNA linear EST 15-NOV-1999
DEFINITION SW14CAK08A08SK Brugia malayi L4 cDNA (SAM99MLM-Bml4) Brugia malayi
ACCESSION CDNA clone SW14CAK08A08 5', mRNA sequence.
VERSION AM172194
KEYWORDS AM172194.1 GI:6431990
SOURCE EST.
ORGANISM Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.

REFERENCE 1 (bases 1 to 50)
AUTHORS Williams, S.A.
TITLE Genes expressed in fourth stage larvae of Brugia malayi
JOURNAL Unpublished (1999)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pbluescript SK.
Location/Qualifiers
1..50

FEATURES

BASE COUNT
ORIGIN
Query Match 41.5%; Score 22.4; DB 10; Length 50;
Best local similarity 72.5%; Pred. No. 2.1e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACTCAGACCTGAGGCTC 45
|||||
DB 44 TAATACGACTCACTATAGGCGCAATGGGTACCGGCCCC 5

RESULT 9
AM160055/c 53 bp mRNA linear EST 05-NOV-1999
LOCUS SW14CAK0605SK Brugia malayi L4 cDNA (SAM99MLM-Bml4) Brugia malayi
DEFINITION CDNA clone SW14CAK0605 5', mRNA sequence.
ACCESSION AM160055
VERSION AM160055.1 GI:6272084
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.

REFERENCE 1 (bases 1 to 53)
AUTHORS Williams, S.A.
TITLE Genes expressed in fourth stage larvae of Brugia malayi
JOURNAL Unpublished (1999)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genomesmith.edu
Email: genomesmith SK.

Seq primer: bluescript SK.
Location/Qualifiers

FEATURES

source

1. .53

/organism="Brugia malayi"

/db_xref="taxon:6279"

/clone="SML4CAK06D05"

/clone_1lb="Brugia malayi L4 CDNA (SAM99MLM-Bml4)"

/dev_stage="larval stage four"

/lab_host="XLI-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of birds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT). Followed by RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genomesmith.edu."

BASE COUNT
ORIGIN

12 a 14 c 17 g 10 t

Query Match 41.5%; Score 22.4; DB 10; Length 53;
Best Local Similarity 72.5%; Pred. No. 2.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAAATAGACTACTATAGGAGACGACACCTGAGGCTC 45
|||||
Db 51 TAAATAGACTACTATAGGAGACGATTTGGTACCGGCCCC 12

RESULT 10
LOCUS

AM041922/c 59 bp mRNA linear EST 15-SEP-1999

DEFINITION SML4CAK02D06SK Brugia malayi L4 CDNA (SAM99MLM-Bml4) Brugia malayi

ACCESSION AM041922 CNA clone SML4CAK02D06 5', mRNA sequence.

VERSION AM041922.1 GI:5900822

KEYWORDS

EST.

SOURCE

ORGANISM

Brugia malayi.

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

Onchocercidae; Brugia.

1 (bases 1 to 59)

REFERENCE

Williams, S.A.

Genes expressed in fourth stage larvae of Brugia malayi

Unpublished (1999)

CONTACT: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genomesmith.edu

Seq primer: bluescript SK.

Location/Qualifiers

1. .59

/organism="Brugia malayi"

/db_xref="taxon:6279"

/clone="SML4CAK02D06"

/clone_1lb="Brugia malayi L4 CDNA (SAM99MLM-Bml4)"

/dev_stage="larval stage four"

/lab_host="XLI-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of birds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by

RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genomesmith.edu."

BASE COUNT
ORIGIN

9 a 18 c 17 g 15 t

Query Match 41.5%; Score 22.4; DB 10; Length 59;
Best Local Similarity 72.5%; Pred. No. 2.3e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAAATAGACTACTATAGGAGACGACACCTGAGGCTC 45
|||||
Db 50 TAAATAGACTACTATAGGAGACGATTTGGTACCGGCCCC 11

RESULT 11
LOCUS

AM172242/c 60 bp mRNA linear EST 15-NOV-1999

DEFINITION SML4CAK06D06SK Brugia malayi L4 CDNA (SAM99MLM-Bml4) Brugia malayi

ACCESSION AM172242 CNA clone SML4CAK06D06 5', mRNA sequence.

VERSION AM172242.1 GI:6432038

KEYWORDS

EST.

SOURCE

ORGANISM

Brugia malayi.

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

Onchocercidae; Brugia.

1 (bases 1 to 60)

REFERENCE

Williams, S.A.

Genes expressed in fourth stage larvae of Brugia malayi

Unpublished (1999)

CONTACT: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genomesmith.edu

Seq primer: bluescript SK.

Location/Qualifiers

1. .60

/organism="Brugia malayi"

/db_xref="taxon:6279"

/clone="SML4CAK06D06"

/clone_1lb="Brugia malayi L4 CDNA (SAM99MLM-Bml4)"

/dev_stage="larval stage four"

/lab_host="XLI-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of birds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by

RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genomesmith.edu."

BASE COUNT
ORIGIN

9 a 20 c 19 g 12 t

Query Match 41.5%; Score 22.4; DB 10; Length 60;
Best Local Similarity 72.5%; Pred. No. 2.3e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAAATAGACTACTATAGGAGACGACACCTGAGGCTC 45
|||||
Db 54 TAAATAGACTACTATAGGAGACGATTTGGTACCGGCCCC 15

RESULT 12

AI096267/c
 LOCUS AI096267 62 bp mRNA linear EST 19-AUG-1998
 DEFINITION SWAMCACC24C05SK Brugia malayi adult male cDNA (SAM94NL-BmAM) Brugia
 malayi cDNA clone SWAMCACC24C05 5', mRNA sequence.
 ACCESSION AI096267
 VERSION AI096267.1 GI:3445056
 KEYWORDS EST.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
 Onchocercidae; Brugia.
 REFERENCE 1 (bases 1 to 62)
 AUTHORS Williams, S.A.
 TITLE Genes expressed in adult males of Brugia malayi
 JOURNAL Unpublished (1995)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences
 Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genome@smith.edu
 Seq primer: Bluescript SK.
 FEATURES
 source
 1..62
 Location/Qualifiers
 /organism="Brugia malayi"
 /strain="TRS labs"
 /db_xref="taxon:6279"
 /clone="SWAMCACC24C05"
 /clone_1lb="Brugia malayi adult male cDNA (SAM94NL-BmAM)"
 /lab_host="XLI-Blue MRF"
 /note="Vector: lambda Uni-zap XR; Site_1: EcoR I; Site_2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from adult males of Brugia malayi
 isolated from jirds and converted to double stranded cDNA
 using reverse transcriptase and oligo(dT) followed by
 RNase H and DNAPol I. The library had 4.6 x 10⁶
 independent recombinants and average insert size was 800
 base pairs. The library was constructed by Noelle Ling.
 The library is available from Dr. S.A. Williams, email
 genome@smith.edu."

BASE COUNT 15 a 15 c 19 g 13 t
 ORIGIN
 Query Match 41.5%; Score 22.4; DB 9; Length 62;
 Best Local Similarity 72.5%; Pred. No. 2.4e+02;
 Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Oy 6 TAATACGACTCATTAGGAGACTCAGACCCCTGAGGCTC 45
 |||||||||||||||||||
 Db 60 TAATACGACTCATTAGGAGACTCAGACCCCTGAGGCTC 21

RESULT 13
 AM159998/c 63 bp mRNA linear EST 05-NOV-1999
 LOCUS AM159998
 DEFINITION SWL4CAK05E03SK Brugia malayi L4 cDNA (SAM99MLW-Bml4) Brugia malayi
 cDNA clone SWL4CAK05E03 5', mRNA sequence.
 ACCESSION AM159998
 VERSION AM159998.1 GI:6272027
 KEYWORDS EST.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
 Onchocercidae; Brugia.
 REFERENCE 1 (bases 1 to 63)
 AUTHORS Williams, S.A.
 TITLE Genes expressed in fourth stage larvae of Brugia malayi
 JOURNAL Unpublished (1999)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genome@smith.edu
 Seq primer: Bluescript SK.
 FEATURES
 source
 1..63
 Location/Qualifiers
 /organism="Brugia malayi"
 /db_xref="taxon:6279"
 /clone="SWL4CAK05E03"
 /clone_1lb="Brugia malayi L4 cDNA (SAM99MLW-Bml4)"
 /dev_stage="larval stage four"
 /lab_host="XLI-Blue MRF"
 /note="Vector: lambda Uni-zap XR; Site_1: Eco RI; Site_2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from L4s isolated from the peritoneal
 cavity of jirds and converted to double-stranded cDNA
 using reverse transcriptase and oligo(dT) followed by
 RNase H and DNA pol I. The library has 2.7 x 10⁵
 independent recombinants and the average insert size is
 approx. 1050bp. The library was constructed by Michelle
 Lizotte-Waniewski. The library is available from Dr. S.A.
 Williams, email: genome@smith.edu."

BASE COUNT 15 a 15 c 20 g 13 t
 ORIGIN
 Query Match 41.5%; Score 22.4; DB 10; Length 63;
 Best Local Similarity 72.5%; Pred. No. 2.4e+02;
 Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Oy 6 TAATACGACTCATTAGGAGACTCAGACCCCTGAGGCTC 45
 |||||||||||||||||||
 Db 60 TAATACGACTCATTAGGAGACTCAGACCCCTGAGGCTC 21

RESULT 14
 AM159945/c 64 bp mRNA linear EST 05-NOV-1999
 LOCUS AM159945
 DEFINITION SWL4CAK04F11SK Brugia malayi L4 cDNA (SAM99MLW-Bml4) Brugia malayi
 cDNA clone SWL4CAK04F11 5', mRNA sequence.
 ACCESSION AM159945
 VERSION AM159945.1 GI:6271974
 KEYWORDS EST.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
 Onchocercidae; Brugia.
 REFERENCE 1 (bases 1 to 64)
 AUTHORS Williams, S.A.
 TITLE Genes expressed in fourth stage larvae of Brugia malayi
 JOURNAL Unpublished (1999)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences
 Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genome@smith.edu
 Seq primer: Bluescript SK.
 FEATURES
 source
 1..64
 Location/Qualifiers
 /organism="Brugia malayi"
 /db_xref="taxon:6279"
 /clone="SWL4CAK04F11"
 /clone_1lb="Brugia malayi L4 cDNA (SAM99MLW-Bml4)"
 /dev_stage="larval stage four"
 /lab_host="XLI-Blue MRF"
 /note="Vector: lambda Uni-zap XR; Site_1: Eco RI; Site_2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from L4s isolated from the peritoneal
 cavity of jirds and converted to double-stranded cDNA

using reverse transcriptase and oligo(dT) followed by
 RNase H and DNA pol I. The library has 2.7 x 10⁵
 independent recombinants and the average insert size is
 approx. 1050bp. The library was constructed by Michelle
 Lizotte-Waniewski. The library is available from Dr. S.A.
 Williams, email: genome@neal.smith.edu."

BASE COUNT

15 a 15 c 21 g 13 t

Query Match

Best Local Similarity 41.5%; Score 22.4; DB 10; Length 64;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY

6 TAATAGACTCAGTATAGGAGACTGAGACCTGAGGCTC 45

Db

62 TAATAGACTCAGTATAGGAGACTGAGGCTC 23

RESULT 15

AM172179/c

66 bp mRNA linear EST 15-NOV-1999
 SW14CAK07G11SK Brugia malayi I4 cDNA (SAM99MLW-Bml4) Brugia malayi

ACCESSION

AM172179

VERSION

AM172179.1 GI:6431975

KEYWORDS

EST.

SOURCE

Brugia malayi.

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

REFERENCE

1 (bases 1 to 66)

AUTHORS

Williams, S.A.

TITLE

Genes expressed in fourth stage larvae of Brugia malayi

JOURNAL

Unpublished (1999)

COMMENT

Contact: Steven A. Williams

FEATURES

Molecular Parasitology

FEATURES

Smith College Department of Biological Sciences

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Department of Biological Sciences, Clark Science Center, Smith

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College, Northampton, MA, 01063, USA

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Tel: 4135853826

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Fax: 4135853786

FEATURES

Email: genome@neal.smith.edu

FEATURES

Seq primer: pbluescript SK.

FEATURES

Location/Qualifiers

FEATURES

1 66

FEATURES

/organism="Brugia malayi"

FEATURES

/db_xref="taxon:6279"

FEATURES

/clone_lib="SW14CAK07G11"

FEATURES

/dev_stage="larval stage four"

FEATURES

/lab_host="XLI-Blue MRF"

FEATURES

/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:

FEATURES

Xho I; Lymphatic filarial nematode parasite of humans.

FEATURES

mRNA was prepared from L4s isolated from the peritoneal

FEATURES

cavity of birds and converted to double-stranded cDNA

Search completed: December 21, 2002, 19:25:02
 Job time : 1673.08 secs

BASE COUNT

17 a 15 c 21 g 13 t

ORIGIN

Query Match

Best Local Similarity 41.5%; Score 22.4; DB 10; Length 66;

Matches

29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY

6 TAATAGACTCAGTATAGGAGACTGAGACCTGAGGCTC 45

Db

63 TAATAGACTCAGTATAGGAGACTGAGGCTC 24

100

Mon Dec 23 08:48:06 2002

us-09-121-239-5.rst

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 739.592 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-5
Perfect score: 24
Sequence: 1 GACCACTGCTGTGTGAACCTCCA 24

Scoring table: IDENTITY:NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_estt:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mem:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	66.7	50	9	AU104202 AU104202
2	15.8	65.8	100	12	BE767056 RC4-WT011
3	15	62.5	97	13	BM139696 GM-40-7A
4	14.6	60.8	58	14	N23403 Yx83h12.s1
5	14.6	60.8	99	10	BE057655 sn05c12.Y
6	14.4	60.0	95	17	BH857328 SALK_0764

7	14.2	59.2	52	9	AI938077 sc41f11.x
8	14.2	59.2	69	17	A2767038 IM056801
9	14	58.3	68	14	B0339757 PIRAM0065
10	14	58.3	73	12	B6820653 602782957
11	14	58.3	75	17	AL767207 Arabidops
12	14	58.3	90	17	A2584799 IM0389M11
13	13.8	57.5	48	10	AV844988 AV844988
14	13.8	57.5	48	17	BE322561 NF006D051
15	13.6	56.7	70	17	BH848620 SALK_0686
16	13.6	56.7	73	10	AM241397 NF006D051
17	13.6	56.7	73	10	AM241397 NF006D051
18	13.6	56.7	94	17	BH216327 1006041H0
19	13.4	55.8	58	9	AT856074 sc31c06.x
20	13.4	55.8	81	10	BE323827 NF006E03P
21	13.4	55.8	82	17	BH218003 1006067F1
22	13.4	55.8	82	9	AA952812 SMTBCEA00
23	13.4	55.8	91	14	T63384 yC07B12.r1
24	13.4	55.8	92	17	A2483748 IM0309M09
25	13.4	55.8	97	13	B1400183 MI-P-AV1-
26	13.2	55.0	40	9	A1180630 uc67f04.x
27	13.2	55.0	57	9	AU255880 AU255880
28	13.2	55.0	60	17	B03761 CSRL-186F7-
29	13.2	55.0	63	17	AQ254801 EP(2)0574
30	13.2	55.0	86	9	AA682708 z187A06.s
31	13.2	55.0	90	10	AM712002 f8a08ne.r
32	13.2	55.0	92	14	BQ763409 EBFC02-SQ
33	13.2	55.0	94	9	AA647390 vq77c09.s
34	13.2	55.0	99	12	BE224750 uz10e03.x
35	13.2	55.0	99	12	T73709 yC53d07.r1
36	13	54.2	70	14	W96947 mT88C03.r1
37	13	54.2	76	17	BH887468 LB005470a.
38	13	54.2	78	17	BH886048 LB005470a.
39	13	54.2	81	17	A2916566 Ps1-7.f1
40	13	54.2	82	9	AA562265 v13404.r
41	13	54.2	82	9	AA562265 v13404.r
42	13	54.2	87	13	BH759199 KG00155-3
43	13	54.2	87	13	B1493713 dF104F06.
44	13	54.2	88	17	A245829 1M0331J19
45	13	54.2	88	17	BH626218 1M07112B0
45	13	54.2	90	17	BH893996 3526_L27

ALIGNMENTS

RESULT 1	AU104202	50 bp	mRNA	linear	EST 30-ANG-2001
LOCUS	AU104202	Sugano Homo sapiens cDNA library	Homo sapiens cDNA clone		
DEFINITION	HEP05745, mRNA sequence.				
ACCESSION	AU104202				
VERSION	AU104202.1	GI:13553723			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata				
AUTHORS	1 (bases 1 to 50)				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
	'H., Okada, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki				
	'I., Nakamura, Y., Suyama, A. and Sugano, S.				
TITLE	Diverse transcriptional initiation revealed by fine, large-scale				
JOURNAL	mapping of mRNA start sites				
MEDLINE	EMBO Rep. 2 (5), 388-393 (2001)				
COMMENT	21270072				
	Contact: Yutaka Suzuki				
	Department of Virology				
	Institute of Medical Science, University of Tokyo				
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan				
	Email: yusuzuki@ims.u-tokyo.ac.jp				
	Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano				
	S. Construction and characterization of a full length-enriched and				
	a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).				
	Location/Qualifiers				

FEATURES

```

source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP05743"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated u937 cells"
BASE COUNT
17 a 14 c 10 g 9 t
ORIGIN

Query Match
Best Local Similarity 66.7%; Score 16; DB 9; Length 50;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACCAACTGCTGTGTAACCTCCA 24
1 ||||| ||||| ||||| |||||
Db 7 GCCCAAGCGTGTGTGTAACCTCCA 30

RESULT 2
BE767056 100 bp mRNA linear EST 19-SEP-2000
LOCUS BE767056
DEFINITION RC4-NT0115-180500-011-c06 NT0115 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE767056
VERSION BE767056.1 GI:10196980
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 100)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-RC4-NT0115-180
500-011-c06&t3=2000-05-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 100.
Location/Qualifiers
1. .100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0115"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site:1: Sma1;
Site:2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
26 a 27 c 23 g 24 t
ORIGIN

Query Match
Best Local Similarity 65.8%; Score 15.8; DB 12; Length 100;
Matches 89.5%; Pred. No. 4e+03;

QY 1 GACCAACTGCTGTGTAACCTCCA 24
1 ||||| ||||| ||||| |||||
Db 7 GCCCAAGCGTGTGTGTAACCTCCA 30

RESULT 2
BE767056 100 bp mRNA linear EST 19-SEP-2000
LOCUS BE767056
DEFINITION RC4-NT0115-180500-011-c06 NT0115 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE767056
VERSION BE767056.1 GI:10196980
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 100)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-RC4-NT0115-180
500-011-c06&t3=2000-05-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 100.
Location/Qualifiers
1. .100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0115"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site:1: Sma1;
Site:2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
26 a 27 c 23 g 24 t
ORIGIN

Query Match
Best Local Similarity 62.5%; Score 15; DB 13; Length 97;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ACCCACTGCTGTGTAACCTCCA 24
1 ||||| ||||| ||||| |||||
Db 62 ACCATATCTCTGTGTAACCTCCA 40

RESULT 4
N23403 58 bp mRNA linear EST 28-DEC-1995
LOCUS N23403
DEFINITION yx83h12.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone
IMAGE:268391 3' similar to SP:s16967 s16967; NADH DEHYDROGENASE ;,
N23403
ACCESSION N23403
VERSION N23403.1 GI:1137553
KEYWORDS EST.

```

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 58)

AUTHORS
Hillier,L., Clark,N., Dubouche,T., Elliston,K., Hawkins,M., Holman
.M., Hulliman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rolloff,T., Soares,M., Tan,F., Trevaaskis,E., Watson
R., Williamson,A., Woldmann,P. and Wilson,R.
The WashU-Merck EST project
Unpublished (1995)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

TITLE
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNLW
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium ([info@image.lnl.gov](#)) for further information.
Trace covered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 728 Std Error: 0.00
Seq primer: m13 -40 forward
High quality sequence stop: 1.
location/Qualifiers

JOURNAL COMMENT

FEATURES
source
1..58
/organism="Homo sapIens"
/db_xref="GDB:3878033"
/db_xref="taxon:9606"
/clone="IMAGE:268391"
/clone_lib="Scorae melanocyte 2NBHM"
/sex="Male"
/lab_type="melanocyte"
/lib_host="PHOB (ampicillin resistant)"
/note="Vector: pRTT3D (Pharmacia) with a modified
polylinker: Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was cloned with a Not I - oIsodIdr) primer [5],
IGTRACACTCTGCAGTCGGCGCCGCCATTTTTTTTGTATTGT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia). Library constructed by Bertie Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony F. Alibino."

BASE COUNT
16 a 11 c 9 g 19 t 3 others

ORIGIN
Query Match Best Local Similarity 60.8%; Score 14.6; DB 14; Length 58;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GACCACA CTGCTG TGTA AACT CC 23
||||| | ||||| |||
Db 49 GACNAANTTG CTTGA AT T TC 27

RESULT 5
BE057655 BE057655 99 bp mRNA linear EST 03-DEC-2001
LOCUS DEFINITION Cm-cl015-8687 5', mRNA sequence.
ACCESSION BE057655.1 GI:8402021
VERSION EST
KEYWORDS soybean,
SOURCE glycine max
ORGANISM Glycyne viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eu dicots;
Spermatocypita; rosids; Fabaceae; Papilionoideae; Phaseoleae;
Kosidae; eurosoids I; fabales; Fabaceae; Papilionoideae; Phaseoleae;
glycine.

REFERENCE	1 (bases 1 to 99)
AUTHORS	Shoemaker,R., Reim,P., Vodkin,L., Erpelting,J., Corvelli,V., Khanna,A., Boll,B., Marra,M., Hillier,L., Knab,T., Martin,J., Beck,C., Wille,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurr,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Materston,R. and Wilson,R.
TITLE	Public Soybean EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contract: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: couteresgen.com Seq primer: 40RP from Gibco.
FEATURES	Location/Qualifiers 1..99 /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-8687" /clone_id="Gm-c1015" /issue_type="Mature flowers, field grown plants" /lab_host="X110-Gold" /note="Vector: plusscript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene plusscript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the plusscript vector. The ligated cDNA fragments were transformed into X110-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."
BASE COUNT	38 a 18 c 18 g 25 t
ORIGIN	
Query Match	60.8%; Score 14.6; DB 10; Length 99;
Best Local Similarity	81.0%; Pred. No. 1.4e+04;
Matches 17: Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY	2 ACCAACTCGTGTGTAACACT 22
Db	46 ACCAACTCATCTGTAAATTC 66
RESULT 6	
BH857328	
LOCUS	BH857328 95 bp DNA linear GSS 08-JUL-2002
DEFINITION	SALK_076431.39.10.x Arabidopsis thaliana YDNA insertion lines
Arabidopsis thaliana genomic clone SALK_076431.39.10.x, DNA sequence.	
ACCESSION	BH857328
VERSION	BH857328.1
KEYWORDS	GI:21708108
SOURCE	GSS
ORGANISM	thale cress. Eukaryotes; thaliana Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicotyledons; rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 95)
AUTHORS	Alonso,J.M., Leissle,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilab,C., Jeske,A., Kaines,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Eckert,J.R.
TITLE	A Sequence-Indexed Library Of Insertion Mutations In The

JOURNAL
COMMENT

Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES
Source

Class: TDNA tagged.
Location/Qualifiers

1. 95
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_076431.39.10.X"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at <http://signal.salk.edu/tdna-protocols.html>"

BASE COUNT 27 a 14 c 21 g 33 t
ORIGIN

Query Match 60.0%; Score 14.4; DB 17; Length 95;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Gy 1 GACCACTCGTGTGTAACCA 24
Db 70 GTCCAGCCGGGATGAACTCCA 93

RESULT 7 52 bp mRNA linear EST 30-NOV-2001
A1938077
LOCUS sc41f11.x1 Gm-cl014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl014-1702 3' similar to TR:064505 064505 PUTATIVE SER/THR
ACCESSION A1938077
VERSION A1938077
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
Glycine.
1 (bases 1 to 52)

REFERENCE
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wille, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuk
R., Riltter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand This clone is
available through: ResGen, Invitrogen Corp. 2130 South Memorial
Parkway Huntville, AL 35801 For further information call: (800
)-533-4363 or contact via email: ccu@resgen.com

FEATURES

Source

Seq primer: primer name ambiguous
High quality sequence stop: 1.
Location/Qualifiers

1. 52
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl014-1702"
/clone_id="Gm-cl014"
/tissue_type="leaves, 2-3 week old seedlings, greenhouse
grown"
/lab_host="DH10B"

/note="Vector: pT73Pac (pT73, Pharmacia); Site 1: EcoRI;
Site 2: HindIII. This cDNA library was constructed from
mRNA isolated from leaves of 2-3 week old greenhouse grown
plants. Complementary DNA was synthesized from mRNA using
a 3' anchored poly (dT) primer. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by
digestion with EcoRI and HindIII. The cDNA fragments were
directionally cloned into the EcoRI-HindIII restriction
site of the pT73-Pac vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker and Dr.
John Erpelting."

BASE COUNT 14 a 10 c 10 g 18 t
ORIGIN

Query Match 59.2%; Score 14.2; DB 9; Length 52;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 1 GACCACTCGTGTGTA 19
Db 28 GACCACTCGTGTGTAA 46

RESULT 8 69 bp DNA linear GSS 16-FEB-2001
A2767038
LOCUS IM0566B01F Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM10566B01 F, DNA sequence.
ACCESSION A2767038
VERSION A2767038
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn, D., Koyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0566 row: B column: 01
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 69.
Location/Qualifiers

FEATURES
Source

1. 69
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

TITLE and Weissshaar, B.
A pipeline for automated high-throughput generation of ESTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines

JOURNAL Unpublished

REFERENCE 2

AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.

TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 75)

AUTHORS Li, Y., Rosso, M., Strizhov, N. and Weissshaar, B.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g62610. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES Location/Qualifiers

SOURCE 1..75

organism="Arabidopsis thaliana"

strain="Columbia 0"

db_xref="taxon:3702"

/clone="GK-217D04-014146"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA from insertions. The DNA fragments(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 22 a 23 c 14 g 16 t

ORIGIN

Query Match 58.3%; Score 14; DB 17; Length 75;
Best Local Similarity 77.3%; Pred. No. 2.4e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ACCAATCGTGTGGAACCTCC 23
1 ||||| 11 |||||

Db 52 AACCACTCTATGGAGACTCC 73
1 ||||| 11 |||||

RESULT 12 A2584799 90 bp DNA linear GSS 13-DEC-2000

LOCUS 1M0389M1R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION C10ne UGCGIM0389M1 R, DNA sequence.

ACCESSION A2584799

VERSION A2584799.1 GI:11706047

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus. 1 (bases 1 to 90)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0389 row: M column: 11
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 90.

FEATURES Location/Qualifiers

SOURCE 1..90

organism="Mus musculus"

strain="C57BL/6J"

db_xref="taxon:10090"

/clone="UGCGIM0389M11"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 30 a 19 c 11 g 30 t

ORIGIN

Query Match 58.3%; Score 14; DB 17; Length 90;
Best Local Similarity 77.3%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CCACTCGTGTGGAACCTCA 24
1 |||| 111 ||||| 11

Db 70 CCAAGAGTGGGTGAACACTCA 49
1 |||| 111 ||||| 11

RESULT 13 AV844988 48 bp mRNA linear EST 08-NOV-2001

LOCUS AV844988 Nori Satoh unpublished cDNA library, cleavage stage embryo

DEFINITION C10ne intestinalis cDNA clone rcl109f08 3', mRNA sequence.

ACCESSION AV844988

VERSION AV844988.1 GI:16822964

KEYWORDS EST.

SOURCE C10ne intestinalis.

ORGANISM Clona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Trochochordata; Ascidiacea; Enterogona; Phlebobranchia; Cloniidae; Clona. 1 (bases 1 to 48)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

TITLE Expressed genes in Clona intestinalis

JOURNAL Unpublished (2000)

COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.


```

FEATURES
  source
    Location/Qualifiers
      1..48
      /organism="Clona intestinalis"
      /db_xref="taxon:7719"
      /clone="rcic109f08"
      /clone_lib="Nori Satoh unpublished cDNA library, cleavage
      stage embryo"
      /tissue_type="whole animal"
      /dev_stage="cleavage stage embryo"
      /note="Vector: pBluescript SK"
BASE COUNT      8 a      11 c      18 g      9 t      2 others
ORIGIN
  Query Match      57.5%; Score 13.8; DB 10; Length 48;
  Best Local Similarity 88.2%; Pred. No. 2.5e+04;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 CTCGTGTGTAACCTCC 23
Db      3 CTCGTGTGTAACCTCC 19

RESULT 14
LOCUS      BE322561
DEFINITION NP006D05IN1F1043 Insect herbivory Medicago truncatula cDNA clone
VERSION      BE322561
KEYWORDS
SOURCE
ORGANISM
  Medicago truncatula
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
  Medicago.
  1 (bases 1 to 75)
REFERENCE
  Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores
  H.R., Inman, J.T., Weller, J.W. and May, G.D.
  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
  Medicago truncatula insect herbivory library
  Unpublished (2000)
  On Jul 14, 2000 this sequence version replaced gi:9196338.
  Contact: Korth K
  Dept. of Plant Pathology
  University of Arkansas
  217 Plant Science Building, Fayetteville, AR 72701, USA
  Tel.: 501 575 5191
  Fax: 501 575 7601
  Email: Kkorth@comp.uark.edu
  Medicago Genome Initiative accession: MGI:S:25300
  Insert Length: 910 Std Error: 0.00
  Plate: 006 row: D column: 05
  Seq primer: TCACACAGGAAACGCTATGAC.
  Location/Qualifiers
    1..75
    /organism="Medicago truncatula"
    /db_xref="taxon:3880"
    /clone="NF006D05IN"
    /clone_lib="Insect herbivory"
    /tissue_type="local and systemic leaves"
    /dev_stage="mature"
    /note="Vector: lambda zap; Library was produced from fully
    expanded M. truncatula leaves of plants fed upon by
    Spodoptera exigua (beet armyworm) for 24 hours. Systemic
    (undamaged leaves from injured plants) and wounded leaves
    were harvested and pooled."
BASE COUNT      24 a      18 c      14 g      19 t
ORIGIN
  Query Match      57.5%; Score 13.8; DB 10; Length 75;
  Best Local Similarity 88.2%; Pred. No. 3e+04;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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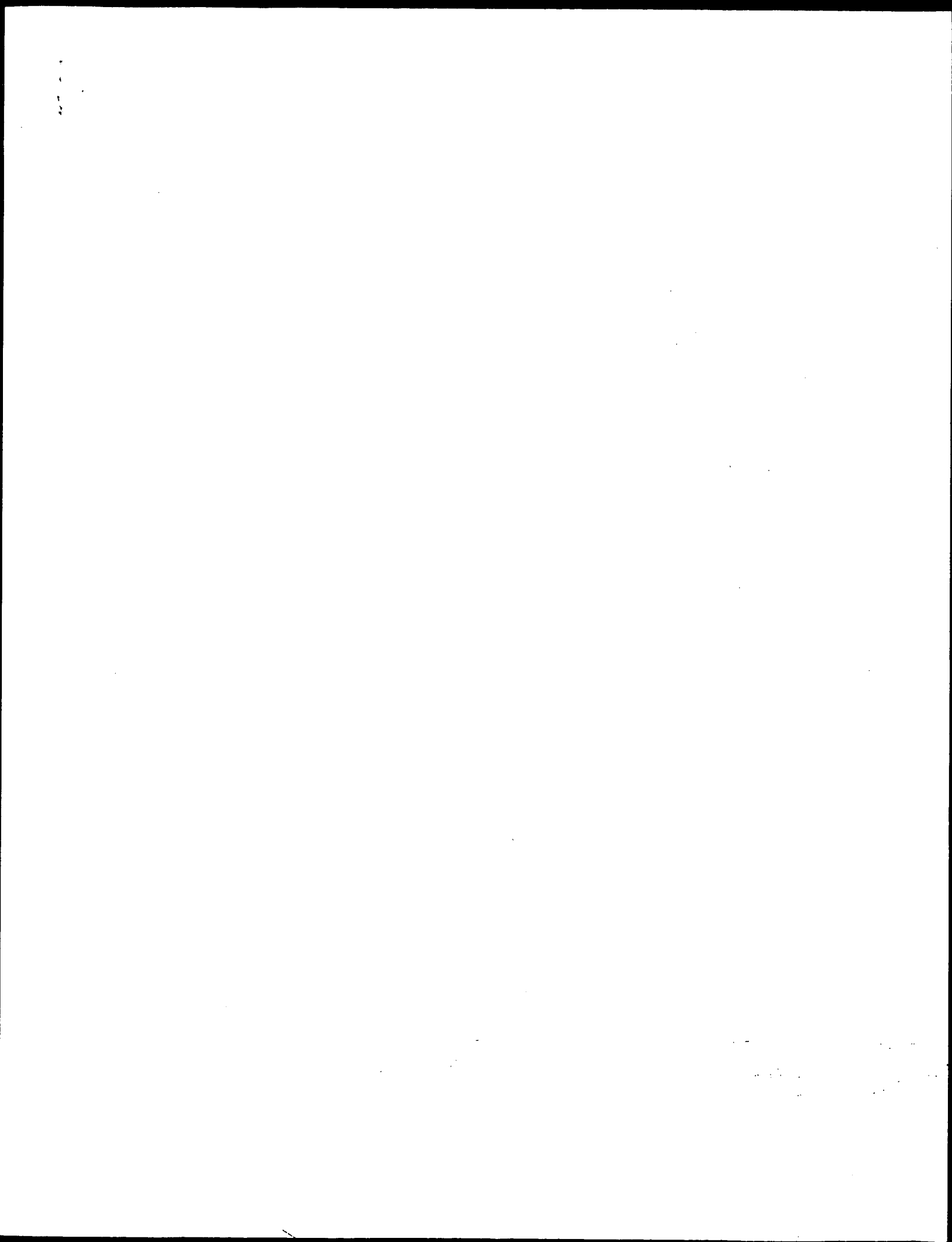
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Qy      8 TCGTGTGTAACCTCCA 24
Db      48 TCGTGTGTAACCTCCA 64

RESULT 15
LOCUS      BH848620
DEFINITION BH848620 20.30 x Arabidopsis thaliana TDNA insertion lines
  Arabidopsis thaliana genomic clone SALK_068609.20.30.x, DNA
  sequence.
  70 bp
  DNA
  linear
  GSS
  13-JUN-2002
ACCESSION      BH848620
VERSION      BH848620.1 GI:21419491
KEYWORDS
SOURCE
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
  1 (bases 1 to 70)
REFERENCE
  Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab
  C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
  Zimmerman, J., and Ecker, J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
  Unpublished (2001)
  Contact: Joseph R. Ecker
  Salk Institute Genomic Analysis Laboratory (SIGAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: eckersalk@u
  This is single pass sequence recovered from the left border of
  TDNA. This sequence lies within an annotated intron of At3g50700.
  Class: TDNA tagged.
  Location/Qualifiers
    1..70
    /organism="Arabidopsis thaliana"
    /strain="Columbia 0"
    /db_xref="taxon:3702"
    /clone="SALK_068609.20.30.x"
    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
    /note="PCR was performed on Arabidopsis thaliana lines
    each of which contains one or more TDNA insertion
    elements. The resultant fragment for each line was
    directly sequenced to determine the genomic sequence at
    the site of insertion. Details of the protocols used can
    be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      27 a      20 c      7 g      16 t
ORIGIN
  Query Match      56.7%; Score 13.6; DB 17; Length 70;
  Best Local Similarity 80.0%; Pred. No. 3.6e+04;
  Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  Qy      5 AACTCGTGTGTAACCTCCA 24
  Db      41 AATCGTATTAAGAACTCCA 60

```

Search completed: December 21, 2002, 19:25:16
 Job time: 753.592 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 770.408 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-9
Perfect score: 25
Sequence: 1 GACGTCCACACATTCGCGTGACC 25

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seg length: 0
Maximum DB seg length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estom:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pla:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtdi:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.6	66.4	70	A1216035	q10e11.x
C 2	15.2	60.8	88	Bj059813	Bj059813
C 3	15	60.0	88	A1883598	A1883598
C 4	14.8	59.2	100	A1006829	ua74e03.r
C 5	14.4	57.6	54	BG020892	df16h09.x
C 6	14.4	57.6	78	AA999832	cv04e02.s

C 7	14.2	56.8	28	A2483948	1M0309119
C 8	14.2	56.8	17	B1736494	B1736494
C 9	14.2	56.8	90	A2474370	1M0290123
C 10	14.2	56.8	94	AA623040	AA623040
C 11	14.2	56.8	92	TA271C040	TA271C040
C 12	14.2	56.8	64	TA271C040	TA271C040
C 13	14.2	56.8	64	TA271C040	TA271C040
C 14	14.2	56.8	64	TA271C040	TA271C040
C 15	14.2	56.8	64	TA271C040	TA271C040
C 16	14.2	56.8	64	TA271C040	TA271C040
C 17	14.2	56.8	64	TA271C040	TA271C040
C 18	14.2	56.8	64	TA271C040	TA271C040
C 19	14.2	56.8	64	TA271C040	TA271C040
C 20	14.2	56.8	64	TA271C040	TA271C040
C 21	14.2	56.8	64	TA271C040	TA271C040
C 22	14.2	56.8	64	TA271C040	TA271C040
C 23	14.2	56.8	64	TA271C040	TA271C040
C 24	14.2	56.8	64	TA271C040	TA271C040
C 25	14.2	56.8	64	TA271C040	TA271C040
C 26	14.2	56.8	64	TA271C040	TA271C040
C 27	14.2	56.8	64	TA271C040	TA271C040
C 28	14.2	56.8	64	TA271C040	TA271C040
C 29	14.2	56.8	64	TA271C040	TA271C040
C 30	14.2	56.8	64	TA271C040	TA271C040
C 31	14.2	56.8	64	TA271C040	TA271C040
C 32	14.2	56.8	64	TA271C040	TA271C040
C 33	14.2	56.8	64	TA271C040	TA271C040
C 34	14.2	56.8	64	TA271C040	TA271C040
C 35	14.2	56.8	64	TA271C040	TA271C040
C 36	14.2	56.8	64	TA271C040	TA271C040
C 37	14.2	56.8	64	TA271C040	TA271C040
C 38	14.2	56.8	64	TA271C040	TA271C040
C 39	14.2	56.8	64	TA271C040	TA271C040
C 40	14.2	56.8	64	TA271C040	TA271C040
C 41	14.2	56.8	64	TA271C040	TA271C040
C 42	14.2	56.8	64	TA271C040	TA271C040
C 43	14.2	56.8	64	TA271C040	TA271C040
C 44	14.2	56.8	64	TA271C040	TA271C040
C 45	14.2	56.8	64	TA271C040	TA271C040

ALIGNMENTS

RESULT 1
A1216035/c 70 bp mRNA linear EST 30-NOV-1998
LOCUS A1216035
DEFINITION q10e11.x1 Scores: NFI.T.GBC.S1 Homo sapiens CDNA clone
IMAGE:1844300 3' similar to TR:Q1513 Q1513 PROCOLAEN
C-PROTEINASE ENHANCER PROTEIN PRECURSOR. [1] : contains TAR1, t3 TAR1
repetitive element ;, mRNA sequence.

ACCESSION A1216035.1 GI:3785076
VERSION 1
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 70)
REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Unpublished (1997)
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Email: cgapb-remail@nci.nih.gov
This clone is available royalty-free through LINT ; contact the
IMAGE Consortium (InfoImage.Lint.gov) for further information.
Trace considered overall poor quality
Insert Length: 2459 Std Error: 0.00
Seq primer: -400p from Glbco
High quality sequence stop: 1.
Location/Qualifiers
1. .70

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1844300"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /lab_host="DH108"
 /note="Organ: pooled; Vector: pT7D-Pac (Pharmacia) with a modified polylinker; Site: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCL-GAP, GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 726408-728711, and 729096-731399. Subtraction by Bento Soares and W. Fatima Bonaldo." 15 t 1 others

Query Match 66.4%; Score 16.6; DB 9; Length 70;
 Best Local Similarity 82.6%; Pred. No. 4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CTGCGACACATTCGGTGACC 25
 Db 59 CTGCGCAACACACTCGCTGAAC 37

RESULT 2
 BJO59813/c 88 bp mRNA linear EST 11-DEC-2001
 LOCUS BJO59813
 DEFINITION laevis cdna clone X1063p11 5', mRNA sequence.
 ACCESSION BJO59813
 VERSION BJO59813.1 GI:17493153
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis

REFERENCE
 AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae; Xenopodinae; Xenopus.
 1 (bases 1 to 88)
 Kikuyama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara

TITLE
 JOURNAL
 COMMENT Expressed genes in X. laevis embryo
 Unpublished (2001)
 Contact: Tadashi Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES
 source
 Location/Qualifiers
 1..88
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_image="X1063p11"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud library"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI. cDNAs were oligo-dT primed and directionally cloned. Staging and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)." 23 a 21 c 20 g 23 t 1 others

BASE COUNT 23 a 21 c 20 g 23 t 1 others
 ORIGIN
 Query Match 60.8%; Score 15.2; DB 13; Length 88;
 Best Local Similarity 85.0%; Pred. No. 1.6e+04;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6 TTCACACATTCGGTGACC 25
 Db 24 TTCACACATTCGGTGACC 5

RESULT 3
 A1883598/c 88 bp mRNA linear EST 07-JUN-2001
 LOCUS A1883598
 DEFINITION f66g12.y1 zebrafish Mashu MPIMG EST Danio rerio cDNA clone
 IMAGE:3726406 5' similar to TR:P97867 P97867 TRANSLATION REPRESSOR
 NAT1.; mRNA sequence.
 ACCESSION A1883598
 VERSION A1883598.1 GI:5588762
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio

REFERENCE
 AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 88)
 Clark, M., Johnson, S.L., Lebrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, R., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Waller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R., Rither, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 Mashu zebrafish EST Project 1998
 Unpublished (1998)
 JOURNAL
 COMMENT Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbratfish@wustl.edu
 CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResourceCenter@primaridenbank, Berlin, Germany (web address: www.rzpd.de)
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: 13 bp from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..88
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone_image="3726406"
 /clone_lib="zebrafish Mashu MPIMG EST"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield stage embryos"
 /lab_host="X11-blue MRP"
 /note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer double-stranded cDNA was ligated to Sal I adaptors (BRL), sites of the pSPOR1 vector (BRL). Library was constructed by Matthew Clark (Lebrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST hybridization were selected following oligonucleotide zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were

sequence.
 accession AA99832 GI:3190387
 version AA99832.1
 keywords EST.
 source human.
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 reference 1 (bases 1 to 78)
 title NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 authors National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 tumor gene index
 journal Unpublished (1997)
 comment Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA library Preparation: M. Bento Soares, Ph.D.
 CDNA library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMW at:
 www.bio.lnlnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40m13 fwd. EF from Amersham
 High quality sequence stop: 1.
 location/Qualifiers
 1..78
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1536346"
 /clone_lib="NCI-CGAP_K1d3"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT7T3D-Pac (pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I oligo(dT) primer,
 double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT7T3 vector. mRNA
 source: 2 pooled kidneys. Library went through one round
 of normalization. Library constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT 13 a 32 c 17 g 16 t
 ORIGIN

Query Match 57.6%; Score 14.4; DB 9; Length 78;
 Best Local Similarity 75.0%; Pred. No. 3.4e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ACTGTCACAGCATTCGCTGACC 25
 |||||
 Db 42 ACGCTCCTCCGCGATCCGCTGAGC 65

RESULT 7
 AZ483948/c 28 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0309J19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0309J19 R, DNA sequence.
 accession AZ483948
 version AZ483948.1 GI:10648274
 keywords GSS.
 source house mouse.
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 reference 1 (bases 1 to 28)
 authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
 Unpublished (2000)
 comment Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0309 row: 3 column: 19
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 location/Qualifiers
 1..28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="UUGC1M0309J19"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi14732114|gb|AF129072.1), a copy number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 8 g 6 t
 ORIGIN

Query Match 56.8%; Score 14.2; DB 17; Length 28;
 Best Local Similarity 84.2%; Pred. No. 3.3e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTGTCCACAGCATTCGCT 21
 |||||
 Db 25 CTGTCCACAGCATTCGAT 7

RESULT 8
 B1736494/c 80 bp mRNA linear EST 20-SEP-2001
 LOCUS 603360142F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5367131 5',
 DEFINITION mRNA sequence.
 accession B1736494
 version B1736494.1 GI:15713507
 keywords EST.
 source house mouse.
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 reference 1 (bases 1 to 80)
 authors NIH-MGC http://mgs.nci.nih.gov/
 title National Institutes of Health, Mammalian Gene Collection (MGC)
 journal Unpublished (1999)
 comment Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov

Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Ince Genes
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://imgc.llnl.gov>
 Plate: LAM11934 row: d column: 12
 High quality sequence: stop: 80.

FEATURES

source
 1 80
 Location/Qualifiers

/organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_image="5367131"
 /clone_lib="NIH_MGC_94"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-Sport6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."

BASE COUNT

8 a 17 c 38 g 17 t

ORIGIN

Query Match 56.8%; Score 14.2; DB 13; Length 80;
 Best Local Similarity 84.2%; Pred. No. 4.2e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACTGTCACAGCATTCGCC 20
 ||||| ||||| ||||| |||||
 Db 61 ACTGGCACAGCACATCCGC 43

RESULT 9

AZ474370 90 bp DNA linear GSS 04-OCT-2000
 LOCUS AZ474370.1
 DEFINITION "10290L23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0290L23 R, DNA sequence."
 accession AZ474370.1 GI:10632495
 VERSION
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0290 row: L column: 23
 Seq primer: CACACAGCAACACACTATGACC
 Class: plasmid ends
 High quality sequence stop: 90.
 Location/Qualifiers

FEATURES

source
 1. 90
 Location/Qualifiers

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="UUGC1M0290L23"

BASE COUNT

30 a 21 c 19 g 20 t

ORIGIN

Query Match 56.8%; Score 14.2; DB 17; Length 90;
 Best Local Similarity 84.2%; Pred. No. 4.3e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACTGTCACAGCATTCGCC 20
 ||||| ||||| ||||| |||||
 Db 88 AATGTCACAGCATTCGCC 70

RESULT 10

AA622040 94 bp mRNA linear EST 31-OCT-1997
 LOCUS AA622040.1
 DEFINITION "nq23c02.s1 NCI-CGAP Col10 Homo sapiens cDNA clone IMAGE:1144706 3'
 similar to TR:G861464 G861464 BOVINE LEUKEMIA VIRUS CELL RECEPTOR
 ;, mRNA sequence."
 accession AA622040
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/bdrp/image/image.html
 Trace considered overall poor quality
 Insert Length: 1216 Std Error: 0.00
 Seq primer: -40m13 fwd. BT from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source
 1. 94
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1144706"
 /clone_lib="NCI-CGAP_Col10"

```

/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/organism="Trypanosoma brucei"
/modified_polylinker="1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo (N-Soares4)."
BASE COUNT      22 a      21 c      31 g      20 t
ORIGIN
Query Match      56.8%; Score 14.2; DB 9; Length 94;
Best Local Similarity 84.2%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTCCACAGCATTCGCGTG 22
||||| ||| ||||| ||
Db 61 TGTGCACATCATTCGCGTG 43

RESULT 11
TA271C04Q      62 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 271c04, reverse sequence,
DEFINITION     genomic survey sequence.
ACCESSION      AL488248
VERSION        AL488248.1 GI:11864100
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei.
ORGANISM       Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 62)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT         Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREV927/4 GYrat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: neilsavedelgr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. 62
/organism="Trypanosoma brucei"
/strain="TREV927"
/db_xref="taxon:5691"
/clone="271c04"
BASE COUNT      15 a      13 c      19 g      15 t
ORIGIN
Query Match      56.0%; Score 14; DB 17; Length 62;
Best Local Similarity 77.3%; Pred. No. 4.8e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTG 22
||||| ||| ||||| ||
Db 32 GACTGTACACACCTTCACATG 53

```

```

RESULT 12
CNS03C5U/c      64 bp      DNA      linear      GSS 15-MAY-2000
LOCUS          Tetradon nigroviridis genome survey sequence pCC-ori end of clone
DEFINITION     013p19 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION      AL237387.1 GI:7896522
VERSION        AL237387
KEYWORDS       GSS; genome survey sequence.
SOURCE         Tetradon nigroviridis.
ORGANISM       Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes;
Tetraodontidae; Tetradon.
1 (bases 1 to 64)
Roest-Criollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 64)
Roest-Criollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Unpublished
3 (bases 1 to 64)
Genoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
Location/Qualifiers
1. 64
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="013p19"
/clone_lib="G"
/note="Genoscope sequence ID : C0B6013CHI0SP1-end :
pCC-ori"
BASE COUNT      8 a      18 c      22 g      15 t      1 others
ORIGIN
Query Match      56.0%; Score 14; DB 17; Length 64;
Best Local Similarity 77.3%; Pred. No. 4.8e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TGTCCACAGCATTCGCGTGACC 25
||||| ||| ||||| ||
Db 63 TTTCCAAACATTCGCGTGACC 42

RESULT 13
AM423872      78 bp      mRNA      linear      EST 03-DEC-2001
LOCUS          sb57b04.y1 Gm-cl015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION     Gm-cl015-3848 5', mRNA sequence.
ACCESSION      AM423872
VERSION        AM423872.1 GI:6951804
KEYWORDS       EST.
SOURCE         soybean.
ORGANISM       Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 78)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna

```


TITLE
JOURNAL
COMMENT

Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estest@wustl.edu
This clone is available through: Resgen, Invitrogen Corp, 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-933-4363 or contact via email: coudresgen.com
Insert Length: 289 Std Error: 0.00
Seq primer: -40RP from Glibco.

FEATURES

source

1. .78

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-3848"

/clone_id="Gm-c1015"

/issue_type="Mature flowers, field grown plants"

/lab_host="X110-Gold"

/note="Vector: pBluescript II XE; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pluescript II
XR cDNA library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pluescript vector. The ligated cDNA fragments were
transformed into X110-gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelting."

BASE COUNT

29 a 24 g 18 t

ORIGIN

Query Match 56.0%; Score 14; DB 10; Length 78;
Best Local Similarity 77.3%; Pred. No. 5e+04;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CTGTCCAGCATTCGCTGAC 24

Db 71 CTGTCTCAGCATTCCTCTGTC 50

RESULT 14

HSMC26D02/c 88 bp DNA linear GSS 29-MAR-1997

LOCUS

H.sapiens DNA for trapped exon (ID HMC26D02), genomic survey

DEFINITION

sequence.

ACCESSION

X88221 GI:1437838

VERSION

GSS.

KEYWORDS

Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ORGANISM

REFERENCE

AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 88)
Cloning of trapped exons from human chromosome 21

AUTHORS

Antonarakis, S.E.

TITLE

Direct Submission

JOURNAL

Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

Medical Genetics, University and Cantonal Hospital of Geneva, CMU,
I rue Michel-Servet, 1211 Geneva, SWITZERLAND
3 (bases 1 to 88)
Chen, H., Chast, R., Rossier, C., Morris, M.A., Laliot, M.D. and
Antonarakis, S.E.
Cloning of 559 potential exons of genes of human chromosome 21 by
exon trapping
Genome Res. 6 (8), 747-760 (1996)
97011340
8858350

FEATURES

source

1. .88

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/note="trapped exon"

BASE COUNT

14 a 19 c 34 g 18 t 3 others

ORIGIN

Query Match 56.0%; Score 14; DB 17; Length 88;
Best Local Similarity 77.3%; Pred. No. 5.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 TGTCACAGCATTCGCTGACC 25

Db 55 TGACACAGCATTCGCTGACC 34

RESULT 15

AA572309 90 bp mRNA linear EST 27-AUG-1997

LOCUS

v152909.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:975904 5' similar to gb:M1305 Mouse type I epidermal keratin
mRNA clone pKSC-50, 3' (MOUSE);, mRNA sequence.

DEFINITION

ACCESSION

AA572309.1 GI:2345504

VERSION

EST.

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 90)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:556632
Seq primer: -28m13 rev1 ET from Amer sham.

FEATURES

source

1. .90

/organism="Mus musculus"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:975904"

/clone_id="Stratagene mouse skin (#937313)"

/sex="females"

/issue_type="whole skin"

/dev_stage="11 weeks old"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: skin; Vector: pluescript SK-; Site 1: EcoRI"

; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
 dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
 adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'
 BASE COUNT 19 a 12 c 29 g 30 t
 ORIGIN

Query Match 56.0%; Score 14; DB 9; Length 90;
 Best Local Similarity 77.3%; Pred. No. 5.2e+04;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACTGTCCACAGCATTCGCTG 22
 |||||
 Db 68 GCCTCTCCCCAGCATTCCTATG 47

Search completed: December 21, 2002, 19:25:29
 Job time : 783.408 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 616.327 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-13
Perfect score: 20
Sequence: 1 CAAAGAGAGAGAGAGAGAG 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpi:*
7: em_estlro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_huv:*
20: em_gss_pln:*
21: em_gss_vft:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.2	76.0	50	9	AU107625 AU107625
2	14.8	74.0	82	9	AA888583 AU107625
3	14.4	72.0	83	17	AA888583 of9008.s
4	14.4	72.0	95	14	AA888583 of9008.s
5	14.2	71.0	52	17	AA888583 of9008.s
6	14.2	71.0	53	17	AA888583 of9008.s

C	7	14.2	71.0	70	9	AA255635	AA255635 z531f07.r
	8	14.2	71.0	76	17	A2497409	A2497409 LM0384E14
	9	14.2	71.0	85	9	AA495306	AA495306 fa01a07.r
	10	14.2	71.0	95	17	TA9C09P	AL451917 T. brucei
	11	14.2	71.0	96	17	AF219048	AF219048 AF219048
	12	14.2	71.0	98	9	A1606834	A1606834 v416b08.x
	13	14.2	71.0	98	9	A1606834	H53725 yu38f12.x1
	14	13.8	69.0	42	14	AA915419	AA915419 v230a10.r
	15	13.8	69.0	51	9	AA496604	AA496604 zv38f05.r
	16	13.8	69.0	70	9	A1544943	A1544943 fb69f02.y
	17	13.8	69.0	70	9	AA983411	AA983411 or45d03.s
	18	13.8	69.0	85	9	AA691847	AA691847 vt05e10.r
	19	13.8	69.0	86	13	BT644202	BT644202 603046069
	20	13.8	69.0	89	17	BH413912	BH413912 1007035C0
	21	13.8	69.0	86	9	AA257631	AA257631 MBLS74H3
	22	13.8	69.0	96	14	B0758134	B0758134 ERMa01.S0
	23	13.8	69.0	100	17	BT478874	BT478874 952002E10
	24	13.6	68.0	33	17	A2363972	A2363972 1M0066C11
	25	13.6	68.0	46	17	A2846167	A2846167 2M0164D15
	26	13.6	68.0	76	9	AA261741	AA261741 v851f08.r
	27	13.6	68.0	82	17	A2830488	A2830488 2M0109F17
	28	13.6	68.0	86	9	AA453618	AA453618 z48b03.s
	29	13.6	68.0	89	17	A2920263	A2920263 1006019A1
	30	13.6	68.0	92	17	AA920051	AA920051 v963h10.r
	31	13.6	68.0	93	17	BH792057	BH792057 SALK_0625
	32	13.6	68.0	96	17	BH405867	BH405867 RPTC-23-8
	33	13.6	68.0	100	14	BQ250094	BQ250094 TA225009H
	34	13.6	68.0	100	17	BH877600	BH877600 hr39d05.b
	35	13.4	67.0	28	17	TA130B12P	TA130B12P T. brucei
	36	13.4	67.0	50	9	AU105451	AU105451 AU105451
	37	13.4	67.0	65	17	AF149510	AF149510 AF149510
	38	13.4	67.0	77	9	AA064271	AA064271 m148h12.r
	39	13.2	66.0	42	17	A2812501	A2812501 2M0079P08
	40	13.2	66.0	49	17	BH846378	BH846378 SALK_0075
	41	13.2	66.0	57	17	A2662175	A2662175 1M0541D09
	42	13.2	66.0	64	14	H53642	H53642 yu38g06.s1
	43	13.2	66.0	64	13	BT261721	BT261721 602954044
	44	13.2	66.0	68	9	AA500663	AA500663 AJ500663
	45	13.2	66.0	69	17	A2487201	A2487201 1M0310B12

ALIGNMENTS

RESULT 1	AU107625	50 bp	MRNA	EST 30-AUG-2001
LOCUS	AU107625			
DEFINITION	AU107625 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone			
ACCESSION	RECC00847			
VERSION	AU107625			
KEYWORDS	AU107625.1 GI:13557146			
SOURCE	EST			
ORGANISM	human			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Seese,J., Hata			
JOURNAL	1 (bases 1 to 50)			
MEDLINE	4-6-1. Shirokanedai, Minatoku, Tokyo 108-8639, Japan			
COMMENT	Email: yuzuki@ims.u-tokyo.ac.jp			
	Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,A. and Sugano			
	a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).			
	Location/Qualifiers			

TITLE Analyses of the Chlamydomonas reinhardtii genome: A Model
Author(s) Chalmers, C. W., Davies, J., Hallis, E., Hauser, C.,
 P., McDermott, J. P., Smrager, J., Silflow, C. and Stern, D.
Journal *Journal of Eukaryotic Microbiology*
Volume 42
Issue 1
Pages 1-10
Year 1995
DOI 10.1080/10634269508839571
URL <http://www.tandf.co.uk/journals/1063-4269>

Vascular Plants. Project: 1030
Unpublished (2002)
Contact: Cheryl R. Russell

Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
Location/Dura

Location/Qualifiers
1. .99

/organism="Chlamydomonas reinhardtii"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone.lib="C. reinhardtii CC-1690, Deflagellation
 (normalized), lambda zap ii"
 (note="Vector: plusscript II SK-; Site-1: EcoRI; Site-2:
 XhoI; Deflagellation library, constructed by John Davies
 and Jeffrey McDermott, combines cDNAs from CC-1690 cells
 which had been re-synthesizing flagella for 15, 30 and 60
 min after being deflagellated by pH shock. polyA mRNA was
 purified from each sample, pooled and cDNA synthesized.
 The cDNA was directionally cloned into lambda zap II
 (Stratagene) in the EcoRI (5') and XhoI (3') sites.
 Plusscript II SK- plasmids were excised from the lambda
 zap clones by superinfection with ExAssist (Stratagene)
 Phage. The library was normalized using method 4 described
 in Ronald et al., (1996) Genome Research 6: 791-806."

AAAGGAGCAGGGAAG 16
||||| |||||
AAAGGAACAGGGAAG 24

Accession	Size	Library	Genome
AZ597805	52 bp	linear	GSS 13-DEC-2000
U04111	10kb	plasmid	musculus genomic

AZ597805.1 GI:11719995
GSS.
house mouse.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus 1 (bases 1 to 52)

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0411 row: F column: 20
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 52.

Location/Qualifiers
1. .52

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0411F20"
/clone.lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab.host="E. Coli strain XL10-gold, Ti-resistant, F-"
/note="vector: PMD42hy; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gii473j114|pb|AF128072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-gold (Stratagene) cells and selected for ampicillin resistance."

```

AAAGGAGCAGGGAAGAAGG 20
 ||| ||| ||||| |||
 AAATGATCATGGAAGAAGG 28

BH638963 55 bp DNA linear
100862603.2EL.y1 1008 - RescueMu Grid 1 Zea mays genomic DNA

BH638963.1 GI:18663620
GSS.
zea mays.
zea mays

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; PACC
clade; Panicoideae; Andropogoneae; zea.
1 (bases 1 to 55)

Unpublished (2001)
Contact: Walbot V

Location/Qualifiers	1. .55

```
/organism="Zea mays"  
/cultivar="mixed background W23/A188/B73"  
/db_xref="taxon:4577"
```

```

/clone.lib="1008 - Rescemu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: leaf; Vector: Rescemu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
Rescemu is a 4.9 kb, modified maize total genomic DNA
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescemu, go to the web
site www.zmld.iastate.edu and follow the links for
'Rescemu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT      13 a      9 c      22 g      11 t
ORIGIN
Query Match      71.0%; Score 14.2; DB 17; Length 55;
Best Local Similarity 84.2%; Pred. No. 4.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 AAAGGACGACGAGGAGAGC 20
        ||||||||| |||||
Db      8 AAAGGACGACGAGGAGAGC 26

RESULT 7
AA255635/c      70 bp mRNA linear EST 13-AUG-1997
LOCUS      zs31f07.f1 NCI.CGAP.GCB1 Homo sapiens cDNA clone IMAGE:686821 5'
DEFINITION similar to SM:YK02.YEAST P36042 HYPOPHYSICAL 21.2 KD PROTEIN IN
TOR2-PAS1 INTERGENIC REGION.; contains element TARI repetitive
element.; mRNA sequence.
AA255635
VERSION      AA255635.1 GI:1892570
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 70)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert Length: 1914 Std Error: 0.00
Seq primer: -28ml3 rev2 fw from Amersham
High quality sequence stop: 1.

FEATURES
Source
1..70
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:686821"
/clone.lib="NCI CGAP GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CHBR). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTACCAATCTGACAGTGGAGCGCGCCCTCAATTTTTTTTTTTTTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors

```

```

(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      0 a      32 c      0 g      38 t
ORIGIN
Query Match      71.0%; Score 14.2; DB 9; Length 70;
Best Local Similarity 84.2%; Pred. No. 4.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 AAAGGACGACGAGGAGAGC 20
        ||||||||| |||||
Db      24 AAAGGAGAGGAGGAGAGG 6

RESULT 8
AA297409      76 bp DNA linear GSS 05-OCT-2000
LOCUS      IM0334E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0334E14 F, DNA sequence.
ACCESSION      AA297409
VERSION      AA297409.1 GI:10674338
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 76)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0334 Row: E Column: 14
Seq primer: CGTGTAAACGACGCGCAGT
Class: Plasmid ends
High quality sequence stop: 76.

FEATURES
Source
1..76
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0334E14"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PMD42uv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473214[9b]/E129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and

```

purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 26 a 10 c 29 g 11 t
 ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 76;
 Best Local Similarity 84.2%; Pred. No. 4.9e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGAGGAGAGAG 20
 ||||| ||||| ||||| |||||
 Db 39 AGAGGAGGAGGAGAGAGG 57

RESULT 9

LOCUS

AA495306 85 bp mRNA linear EST 27-JUN-1997
 fa01807.r1 zebrafish ICRFzfls Danio rerio cDNA clone 1A3 5' similar
 to AF256C9.1 CE01319 PPI ; mRNA sequence.

ACCESSION

AA495306
 VERSION AA495306.1 GI:2225734

KEYWORDS

EST.

SOURCE

zebrafish.

ORGANISM

Danio rerio

REFERENCE

1 (bases 1 to 85)

Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M.,
 Eddy, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G.,
 Jost, S., Kucaba, T., Lacey, M., Le, N., Lennon, G., Martin, J., Moore, B.,
 Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie,
 T., Waterston, R. and Wilson, R.
 Washu Zebrafish EST Project
 Unpublished (1997)

TITLE

zebrafish

JOURNAL

Unpublished (1997)

COMMENT

Contact: Steve Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@wustl.edu
 Steve Johnson lab Internal ID - P1-13 NOTE - For this library, the
 CDNA library represents a position identifier on the original
 CDNA library preparation plate. CDNA library preparation by:
 Clark. CDNA library Arrayed by: Matthew Clark. DNA Sequencing by:
 Washington University Genome Sequencing Center Clone distribution:
 Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare
 Genetik, Berlin Tel +49 30 84 13 1235
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: 17 ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1..85
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone="1A3"
 /clone_lib="zebrafish ICRFzfls"
 /sex="mixed"
 /tissue_type="pooled 26-somite embryos"
 /lab_host="XLI Blue MRF"
 /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
 strand cDNA was primed with a Not I - oligo(dT)15 primer
 13' pGACTAGTCTGATCGGAGCGCCCTTTTCTTTTCTTTT3'1, on
 mRNA from pooled 26 somite zebrafish embryos;
 double-stranded cDNA was ligated to Sal I adaptors (BRL),
 digested with Not I and cloned into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehrach lab, ICRF, London and Max
 Planck Institut fuer Molekulare Genetik, Berlin) and was
 not biochemically normalised. 70,000 clones from this

library were arrayed on high density filters and
 subsequently screened by oligonucleotide hybridization
 fingerprinting to identify unique or minimally redundant
 clones for more intensive analysis."

BASE COUNT 29 a 12 c 24 g 20 t
 ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 85;
 Best Local Similarity 84.2%; Pred. No. 5e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGAGGAGAGAG 20
 ||||| ||||| ||||| |||||
 Db 44 AAACGAGGAGGAGAGAGG 62

RESULT 10

LOCUS

TA9C09P 95 bp DNA linear GSS 13-DEC-2000
 TA9C09P
 T. Brucei sheared genomic DNA clone 9C09, forward sequence, genomic
 survey sequence.

ACCESSION

AL451917
 AL451917.1 GI:11861109

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

ORGANISM

Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE

1 (bases 1 to 95)

Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajadream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhs@sanger.ac.uk
 constructed at the Institute for Genomic Research (TIGR).
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREM927/4 COTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

TITLE

Trypanosoma

JOURNAL

Unpublished (1997)

COMMENT

Location/Qualifiers

FEATURES

source

1..95
 /organism="Trypanosoma brucei"
 /strain="TREM927"
 /db_xref="taxon:5691"
 /clone="9C09"

BASE COUNT

38 a 14 c 27 g 16 t

ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 95;
 Best Local Similarity 84.2%; Pred. No. 5e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGAGGAGAGAG 20
 ||||| ||||| ||||| |||||
 Db 54 AAAGGACGAGGAGAGAGG 72

RESULT 11

LOCUS

AF219048 96 bp DNA linear GSS 17-APR-2000
 AF219048 Human Homo sapiens genomic clone B05, DNA sequence.

ACCESSION

AF219048
 VERSION AF219048.1 GI:7581585

KEYWORDS	GSS.
SOURCE	human
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 96)
	Hansher, M., Cross, S., Daniels, M., Lennon, G. and Brook, J.D.
	A transcript map of a 10-Mb region of chromosome 19: A source of
	genes for human disorders, including candidates for genes involved
	in asthma, heart defects, and eye disorders
	Genomics 63 (3), 425-429 (2000)
JOURNAL	20171383
MEDLINE	Contact: Hansher M
COMMENT	Institute of Genetics
	University of Nottingham
	Queen's Medical Center, Nottingham, NG7 2LR, United Kingdom
	Class: exon-trapped.
FEATURES	location/Qualifiers
source	1..96
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="Bd5"
	/clone_id="Human"
	/note="Vector: pMOS Blue"
BASE COUNT	24 a 23 c 35 g 14 t
ORIGIN	
Query Match	71.0%; Score 14.2; DB 17; Length 96;
Best Local Similarity	84.2%; Pred. No. 5e+04;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 CAAGGACGAGGGAAG 19
Db	3 CAAGGTGCATGGGAGA 21
RESULT 12	
LOCUS	A1606834 98 bp mRNA linear EST 21-APR-1999
DEFINITION	vw16b08.x1 Soares_thymus_2NDMT Mus musculus cDNA clone
ACCESSION	A1606834
VERSION	A1606834
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 98)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.
	Email: cgaps-rt@mail.nih.gov
	This clone is available royalty-free through LNLN; contact the
	IMAGE Consortium (info@image.llnl.gov) for further information.
	NCI:657647
	This clone was previously sequenced on the 5' end only, this new
	data is from the 3' end
	High quality sequence stop: 91.
FEATURES	location/Qualifiers
source	1..98
	/organism="Mus musculus"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="IMAGE:1243959"
	/clone_id="Soares_thymus_2NDMT"
	/sex="male"
	/tissue_type="Thymus"
	/dev_stage="4 weeks"
	/lab_host="DH10B"
	/note="Vector: pT73D-Pac (Pharmacia) with a modified

BASE COUNT	25 a	7 c	33 g	33 t
ORIGIN				
Query Match	71.0%;	Score 14.2;	DB 9;	Length 98;
Best Local Similarity	84.2%;	Pred. No. 5.1e+04;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
OY	2	AAGAAGCAGGAGGAGAAGG 20		
	1			
Db	61	ACAGCTGCAGGAGGAGAAGG 79		
RESULT 13				
H53725	49 bp	mRNA	linear	EST 20-SEP-1995
LOCUS	YU8f12c.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone			
DEFINITION	IMAGE2136111 5' similar to SP:S2454 S2454 H84 PROTEIN - ; mRNA sequence.			
ACCESSION	H53725			
VERSION	H53725			
KEYWORDS	H53725.1 GI:993872			
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 49)			
	Chissoe,S., Lennom,G., Becker,M., Bonaldo,M.F., Chiappelli,B., Hillier,L., Dietrich,N., Dubugue,T., Favello,A., Gish,W., Hawkins,M., Hulman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Riklin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Franje,T., Thlermy-Meg,J., Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.			
	Generation and analysis of 280,000 human expressed sequence tags			
	Genome Res. 6 (9), 807-828 (1996)			
TITLE	97044478			
JOURNAL	Contact: Wilson RK			
MEDLINE	Washington University School of Medicine			
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: est@watson.wustl.edu			
	Insert Size: 1213			
	High quality sequence starts: 1			
	High quality sequence stops: 1			
	Source: IMAGE Consortium, LML			
	This clone is available royalty-free through LML; contact the			
	IMAGE Consortium (infoimage.lml.gov) for further information.			
	Trace considered overall poor quality			
	Possible reversed clone: similarity on wrong strand			
	Insert Length: 1213 Std Error: 0.00			
	Seq primer: M13RPI			
	High quality sequence stop: 1.			
FEATURES	location/Qualifiers			
source	1..49			
	/organism="Homo sapiens"			
	/db_xref="GDB:3863030"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:236111"			
	/clone_id="Soares ovary tumor NBHOT"			
	/sex="female"			
	/tissue_type="ovarian tumor"			
	/lab_host="DH10B (ampicillin resistant)"			
	/note="Organ: ovary; Vector: pT773D (Pharmacia) with a			
	modified polylinker site_1: Not I; Site_2: Eco RI; 1st			

OY 1 CAAGGAGCGGGAAGA 17
11 11111111 1111
DB 13 CACAGGAGCGAGAGA 29

Search completed: December 21, 2002, 19:25:40
Job time : 627.327 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 739.592 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-16

Sequence: 24
1 GTGGACATGACCCCTCAGCGG 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estda:*
2: em_estlm:*
3: em_estln:*
4: em_estlv:*
5: em_estov:*
6: em_estol:*
7: em_estro:*
8: em_estc:*
9: gb_estc:*
10: gb_estc:*
11: gb_estc:*
12: gb_estc:*
13: gb_estc:*
14: gb_estc:*
15: em_estlm:*
16: em_estlm:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15.2	69	17	AZ838667 2M0134N22
2	15.2	63.3	91	AA754748 vU20h06.r
3	14.8	61.7	70	AA762759 vV85h12.r
4	14.6	60.8	40	AZ805795 2M0067F20
5	14.6	60.8	65	AZ842595 2M0141F08
6	14.4	60.0	79	BH632587 1007096B0

C	7	14.4	60.0	83	9	AT720123
C	8	14.4	60.0	84	17	BH416484
C	9	14.4	60.0	89	17	AZ922244
C	10	14.2	59.2	42	17	AZ838487
C	11	14.2	59.2	42	17	AZ838487
C	12	14.2	59.2	76	17	AL768539
C	13	14.2	59.2	89	17	AL768539
C	14	14.2	59.2	99	17	AZ858525
C	15	14.2	59.2	99	17	AZ858525
C	16	14.2	59.2	99	17	AZ858525
C	17	14.2	59.2	99	17	AZ858525
C	18	14.2	59.2	99	17	AZ858525
C	19	14.2	59.2	99	17	AZ858525
C	20	14.2	59.2	99	17	AZ858525
C	21	14.2	59.2	99	17	AZ858525
C	22	14.2	59.2	99	17	AZ858525
C	23	14.2	59.2	99	17	AZ858525
C	24	14.2	59.2	99	17	AZ858525
C	25	14.2	59.2	99	17	AZ858525
C	26	14.2	59.2	99	17	AZ858525
C	27	14.2	59.2	99	17	AZ858525
C	28	14.2	59.2	99	17	AZ858525
C	29	14.2	59.2	99	17	AZ858525
C	30	14.2	59.2	99	17	AZ858525
C	31	14.2	59.2	99	17	AZ858525
C	32	14.2	59.2	99	17	AZ858525
C	33	14.2	59.2	99	17	AZ858525
C	34	14.2	59.2	99	17	AZ858525
C	35	14.2	59.2	99	17	AZ858525
C	36	14.2	59.2	99	17	AZ858525
C	37	14.2	59.2	99	17	AZ858525
C	38	14.2	59.2	99	17	AZ858525
C	39	14.2	59.2	99	17	AZ858525
C	40	14.2	59.2	99	17	AZ858525
C	41	14.2	59.2	99	17	AZ858525
C	42	14.2	59.2	99	17	AZ858525
C	43	14.2	59.2	99	17	AZ858525
C	44	14.2	59.2	99	17	AZ858525
C	45	14.2	59.2	99	17	AZ858525

ALIGNMENTS

RESULT 1	AZ838667	69 bp	DNA	linear	GSS 20-FEB-2001
LOCUS	2M0134N22	Mouse 10kb plasmid	UUCGIM library	Mus musculus genomic	
DEFINITION	clone UUCG2M0134N22 F, DNA sequence.				
ACCESSION	AZ838667				
VERSION	AZ838667.1	GI:13008575			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beccorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00				

MGI:639091
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality

1.91

BASE COUNT
ORIGIN

/organism="Mus musculus"
 /strain="C3H"
 /db_xref="taxon:10090"
 /clone="IMAGE:1181243"
 /clone_1ib="Barstead mouse myotubes MPLR5"
 /cell_line="C2C12"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site.1: EcoRI; Site.2: NotI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTTCGATCTCGAATGGAGGCGCCGCCCTTTTCTTTTCTTTTCTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (AAATCGAGCTCTTG), digested with Not I and cloned into the
 library constructed by Bob Barstead. The C2C12 cell line
 (available from ATCC, catalog # CRL-1772) differentiates
 rapidly, forming contractile myotubes and producing
 characteristic muscle proteins."

	Query Match	63.3%	Score 15.2	DB 9	Length 91
	Best Local Similarity	85.0%	Pred NO. 7.8e+03		
	Matches 17	Conservative	0	Mismatches 3	Indels 0
				Gaps	0
QY	3	GGACATGAAGCCCTCAGC	22		
Db	80	GGACATGAGCCCTGCATC	61		

Qy	3	GGACATGAAGCCCTTCAGC	22
Db	19	GGACATGAATCGCTTAGC	38

RESULT 2	
AA754748/c	
LOCUS	91 bp mRNA linear EST 21-JAN-1998
DEFINITION	Vu00g06.r1 Barstead mouse myotubes MPRB5 Mus musculus cDNA clone
ACCESSION	U00861.1 181243 5' similar to WP:2K657.2 CE00433 ; , mRNA sequence.
VERSION	AA754748
DATE	MAY07/98 1 22:00

SOURCE	ORGANISM	REFERENCE	AUTHORS
house mouse.	<i>Mus musculus</i>		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 91)		
	Matta, M., Hillier, L., Allen, M., Bowles, M., Brown, J., et al.		

TITLE	EST
The WashU-HIMI Mouse Project	
Unpublished (1996)	
Contact: Marra M/Mouse Fsm Proje	

Contact: Maira W/Mouse EST Project
Washu-HM1 Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

ORGANISM	REFERENCE	AUTHORS
<i>Mus musculus</i>		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus;		
1 (Passes 1 to 70)		
Marr, M., Hillier, L., Allen, M., Bowles, M., Datta, S., Datta, S., Datta, S.,		

TITLE	JOURNAL	COMMENT
The WashU-HHMI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project

FEATURES

This... mouse@stewartson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAG Consortium (info@image.lnl.gov) for further information.
 MGI:854847
 Seq primer: -28m3 rev1 ET from Amersham.
 Location/Qualifiers
 1..70
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:10090"

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/clone="IMAGE:1229255"
/sex="females"
/tissue.type="whole skin"
/seq.str="11 weeks old"
/lab.host="SOLR (kanamycin resistant)"
/note="organ: skin; Vector: pBluescript SK-; Site: 1: EcoRI
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dr whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; uni-ZAP XR Vector: -5'
adaptor sequence: 5' CTGAGTCTTTTCTTTTCTTTT 3' adaptor
sequence: 5' CTGAGTCTTTTCTTTTCTTTT 3'
BASE COUNT      19 a      22 c      15 g      14 t
ORIGIN
Query Match      61.7%; Score 14.8; DB 9; Length 70;
Best Local Similarity 88.9%; Pred. No. 1.1e+04;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      4      GAACTGATGACCTTCAG 21
Db      46      GATCTTGAAGCCTTCAG 29

RESULT 4
LOCUS      A2805795      40 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION      2M0067F20F Mouse 10kb plasmid UOCCIM library Mus musculus genomic
ACCESSION      A2805795
VERSION      A2805795.1 GI:12966606
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 40)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: F column: 20
Seq primer: CGTTGTAAGCAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1..40
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UOCC2M0067F20"
/clone_1lb="Mouse 10kb plasmid UOCCIM library"
/sex="Male"
/lab.host="E. coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (911473211419b1AF129072.1), a copy number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      12 a      8 c      11 g      9 t
ORIGIN
Query Match      60.8%; Score 14.6; DB 17; Length 40;
Best Local Similarity 81.0%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY      3      GGAACATGATGACCTTCAGC 23
Db      17      GGAACATGATGACCTTCAGC 37

RESULT 5
LOCUS      A2842595      65 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION      2M0141F08F Mouse 10kb plasmid UOCCIM library Mus musculus genomic
ACCESSION      A2842595
VERSION      A2842595.1 GI:13012503
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 65)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0141 row: F column: 08
Seq primer: CGTTGTAAGCAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 65.
Location/Qualifiers
1..65
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UOCC2M0141F08"
/clone_1lb="Mouse 10kb plasmid UOCCIM library"
/sex="Male"
/lab.host="E. coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

```


DEFINITION 1007048D02.2BL.y1 1007 - RescuenMu Grid H Zea mays genomic, DNA sequence.

ACCESSION BH416484

VERSION BH416484.1 GI:17599142

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 84)

Maize genomic sequences found using engineered RescuenMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1007048 column: 28

Class: transposon-tagged.

Location/Qualifiers

1..84

/organism="Zea mays"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/clone_1lb="1007 - RescuenMu Grid H"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: leaf; Vector: RescuenMu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; RescuenMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuenMu, go to the web site 'www.zmbl.laistate.edu' and follow the links for 'RescuenMu', 'Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 16 a 22 c 20 g 26 t

ORIGIN

Query Match 60.0%; Score 14.4; DB 17; Length 84;

Best Local Similarity 75.0%; Pred. No. 1.8e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GTGGAACATGAAGCCCTTCAGCGG 24

||||| 11 11111111

Db 74 GTGGAATAATTACCCCTTCAGCTG 51

RESULT 9

AZ992244

LOCUS 89 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0276N13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION AZ992244

VERSION 2M0276N13R mouse 10kb plasmid UUGC2M library Mus musculus genomic

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 89)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly

JOURNAL

COMMENT

'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert length: 10000 std error: 0.00

Plate: 0276 row: N column: 13

Seq primer: CACACGAGAAACACGATAGCC

Class: plasmid ends

High quality sequence stop: 89.

Location/Qualifiers

1..89

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0276N13"

/clone_1lb="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD22ny; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (911473211419b1AE129072.1) a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 17 a 18 c 20 g 34 t

ORIGIN

Query Match 60.0%; Score 14.4; DB 17; Length 89;

Best Local Similarity 75.0%; Pred. No. 1.8e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GTGGAACATGAAGCCCTTCAGCGG 24

||||| 11 11111111

Db 42 GTGGCAGCTTGATGCTTTCAGCGG 65

RESULT 10

AZ838487

LOCUS 42 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0134N09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION AZ838487

VERSION 2M0134N09R mouse 10kb plasmid UUGC1M library Mus musculus genomic

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly

TITLE
JOURNAL
COMMENT

'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: N column: 09
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 42.

FEATURES
source
1. .42
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UGCC2M0134N09"
/clone_lib="Mouse 10kb plasmid UGCC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
12 a 7 c 12 g 11 t

Query Match 59.2%; Score 14.2; DB 17; Length 42;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GGAACATGAAGCCCTTCAG 21
|||||
Db 18 GGAACATGAATCGCTTCG 36

RESULT 11
LOCUS A2954607 42 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0220B23P Mouse 10kb plasmid UGCC2M 1library Mus musculus genomic
clone UGCC2M0220B23 F, DNA sequence.
ACCESSION A2954607
VERSION A2954607.1 GI:13825834
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

TITLE
JOURNAL
COMMENT

'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: B column: 23
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 42.

FEATURES
source
1. .42
Location/Qualifiers

/organism="Mus musculus"
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/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UGCC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
11 a 7 c 10 g 14 t

Query Match 59.2%; Score 14.2; DB 17; Length 42;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GGAACATGAAGCCCTTCAG 21
|||||
Db 19 GGAACATGAATCGCTTCG 37

RESULT 12
LOCUS AL768539 76 bp DNA linear GSS 19-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-075H10-011890,
genomic survey sequence.
ACCESSION AL768539
VERSION AL768539.1 GI:21521658
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Siedler, H.

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: J column: 10
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 99.
Location/Qualifiers

FEATURES

source

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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

27 a 18 c 15 g 39 t

ORIGIN

Query Match 59.28; Score 14.2; DB 17; Length 99;
Best Local Similarity 84.2%; Pred. No. 2.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGAACATGAAGCCCTCAG 21

Db 16 GGAACATGAATCGCTCAG 34

RESULT 15
AZ990610 41 bp DNA linear GSS 27-Apr-2001
LOCUS
DEFINITION 2M0274I23F Mouse 10kb plasmid U06C2M library Mus musculus genomic
clone U06C2M0274I23 F, DNA sequence.
ACCESSION AZ990610
VERSION
KEYWORDS
SOURCE
ORGANISM house mouse.
Mus musculus

REFERENCE
AUTHORS 1 (bases 1 to 41)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0274 row: I column: 23
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers

FEATURES

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/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

11 a 7 c 15 g 8 t

ORIGIN

Query Match 58.3%; Score 14; DB 17; Length 41;
Best Local Similarity 77.3%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGAACATGAAGCCCTCAGCG 24

Db 19 GGAACATGAATCGCTGCGCG 40

Search completed: December 21, 2002, 19:25:49
Job time: 748.592 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 832.041 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-22

Sequence: 1 TCTGACCTTGAGCCCTGAGGCTGAGT 27

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:*
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_ohe:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	15.6	57.8	72	17	FR0010427 F.rubripie
4	15.6	57.8	97	17	BG535415 602563077
5	15.4	57.0	52	17	AZ597394 1M0411B23
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33 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
34 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
35 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
36 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
37 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
38 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
39 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
40 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
41 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
42 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
43 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
44 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x
45 <td>14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td></td>	14.2 <td>52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td></td>	52.6 <td>88</td> <td>9 <td>AI337691 w83d11.x</td> </td>	88	9 <td>AI337691 w83d11.x</td>	AI337691 w83d11.x

ALIGNMENTS

RESULT 1
LOCUS AZ800849 59 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0059602F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0059602 F. DNA sequence.
ACCESSION AZ800849
VERSION AZ800849.1 GI:12953172
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 59)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: 0 column: 02
 Seq primer: CGTGTGTAACGACGCGCAGT
 Class: Plasmid ends
 High quality sequence stop: 59.
 Location/Qualifiers
 1..59

source
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGC2M0059002"
 /clone_1lb="Mouse 10kb plasmid TUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (911473211419b) (AF129072.1) a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

12 a 17 c 13 g 17 t

ORIGIN

Query Match 59.3%; Score 16; DB 17; Length 59;
 Best Local Similarity 79.2%; Pred. No. 4.9e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TGTGACTTTGAGCTCAGGCTCTG 24
 ||||| ||||| ||||| |||||
 Db 7 TGTGCTTCTAGCCTCAAGCTCTG 30

RESULT 2

BE587181

LOCUS

BE587181

DEFINITION

BE587181

ACCESSION

BE587181

VERSION

BE587181.1

KEYWORDS

EST.

SOURCE

rye.

ORGANISM

rye.

REFERENCE

1 (bases 1 to 100)

AUTHORS

Anderson, O.D., Butler, E., Chao, S., Gustafson, J.P., Han, P.S., Hsia, T.C., Kang, Y., Izzo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.

TITLE

The structure and function of the expressed portion of the wheat genomes - Aluminum-stressed root tip cDNA library from rye (Secale cereale)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105555773
 Fax: 5105555818
 Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
 Seq primer: M13 reversed primer.
 Location/Qualifiers
 1..100

source
 /organism="Secale cereale"
 /cultivar="Bianco"
 /db_xref="taxon:4550"
 /clone="WHE0519_D07_H13"
 /clone_1lb="Secale cereale aluminum-stressed root tip cDNA library"
 /tissue_type="Root tip"
 /dev_stage="Seedling"
 /lab_host="E. coli DH2S"
 /note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; Seeds were germinated aseptically on filter paper and transferred to a hydroponic growth system in a growth chamber when the primary root was 1 cm in length. After a 2-day establishment period, seedlings were subjected to a 5 ppm aluminum stress prior to tissue harvest. Plants were grown in an environmental chamber. The tissue, total RNA, and poly(A) RNA were prepared, and a cDNA library was made (Butler and Gustafson) at University of Missouri, Columbia. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT

21 a 19 c 33 g 27 t

ORIGIN

Query Match 59.3%; Score 16; DB 10; Length 100;
 Best Local Similarity 79.2%; Pred. No. 6.2e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 TGACTTGAACCTCAGGCTCTGAG 26
 ||||| ||||| ||||| |||||
 Db 45 TGCCCTTGAGCTCAGGTGTGAG 68

RESULT 3

FR0010427

LOCUS

FR0010427

DEFINITION

FR0010427

ACCESSION

AL001704

VERSION

AL001704.1

KEYWORDS

GSS: genome survey sequence.

SOURCE

Takifugu rubripes.

ORGANISM

Takifugu rubripes.

REFERENCE

1 (bases 1 to 72)

AUTHORS

Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umranta, Y., Williams, G. and Brenner, S.

TITLE

Direct Submision

JOURNAL

Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: bihel@hmp.mrc.ac.uk

COMMENT

Vector: pBluescript II KS
 V type: phagemid
 PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.
 Location/Qualifiers
 1..72

FEATURES

source

ORGANISM

Takifugu rubripes

REFERENCE

1 (bases 1 to 72)

AUTHORS

Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umranta, Y., Williams, G. and Brenner, S.

TITLE

Direct Submision

JOURNAL

Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: bihel@hmp.mrc.ac.uk

COMMENT

Vector: pBluescript II KS
 V type: phagemid
 PRIMER: KS

BASE COUNT

11 a 17 c 21 g 21 t 2 others

ORIGIN

Query Match 57.8%; Score 15.6; DB 17; Length 72;
 Best Local Similarity 81.8%; Pred. No. 8e+03;

RESULT 6	
AA973016	
LOCUS	97 bp mRNA linear EST 20-MAY-1998
DEFINITION	OP2E03.s1 Soares_NFL_T-GBC_ST Homo sapiens CDNA clone T-COMPLEX PROTEIN IMAGE:577884 3' similar to SW:TCFZ_HUMAN F40227
ACCESSION	AA973016
VERSION	AA973016.1 GI:3148196
KEYWORDS	
SOURCE	human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 97)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: 40m13 fwd. EF from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1577884"
 /clone_1lb="Soares_NFL-T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pF713D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbH119w, testis NHT, and B-cell NCI-CGAP GC81) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 27 a 20 c 26 g 24 t
 ORIGIN
 Query Match 56.3%; Score 15.2; DB 9; Length 97;
 Best Local Similarity 85.0%; Pred. No. 1.4e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TTGAGCTTGGAGCGTCGAGG 20
 ||||| ||||| ||||| |||||
 Db 8 TCTGGCTTTGACCTCAGG 27
 RESULT 7
 BO566275/c 98 bp mRNA linear EST 19-JUN-2002
 LOCUS g156g02.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
 DEFINITION clone g156g02.5, mRNA sequence.
 ACCESSION BO566275
 VERSION BO566275.1 GI:21469592
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 98)
 AUTHORS Kachar, B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharben@nid.nih.gov
 Plate: 56 row 9 column: 02
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers

source
 1..98
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g156g02"
 /clone_1lb="Mouse Organ of Corti cDNA pluescript"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13".
 /note="Organ: Organ of Corti. Vector: pluescript. The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was clipped away, stria vascularis epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dGTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with Xho I adaptors in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Palo Alto, CA) and Clontech Chroma Spin-1000 (Clontech, Upstate, Sweden) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon filtration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. The 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGAC) and 258 Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 23 a 20 c 29 g 26 t
 ORIGIN
 Query Match 56.3%; Score 15.2; DB 14; Length 98;
 Best Local Similarity 85.0%; Pred. No. 1.4e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 8 TTGAGCTTGGAGCGTCGAGT 27
 ||||| ||||| ||||| |||||

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldi, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnlnl.gov/dbip/image/image.html
 Seq primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 73.
 Location/Qualifiers

1. 89
 /organism="Homo sapiens"
 /db_xref="GDB:6035132"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:815655"
 /clone_id="NCI-CGAP.GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="vector: pMT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20⁺, 19D-1), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGACAGCGGCGGCGCTCTTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldi."
 BASE COUNT 27 a 24 c 22 g 16 t
 ORIGIN

Query Match 54.8%; Score 14.8; DB 9; Length 89;
 Best Local Similarity 88.9%; Pred. No. 2e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 7 TTTGAGCCTCAGGCTG 24
 ||||| ||||| |||||
 Db 61 TTTGAGCCTCAGGCTG 44

RESULT 11
 A1594823 76 bp mRNA linear EST 21-APR-1999
 LOCUS v18e08.x1 StrataGene mouse heart (#937316) Mus musculus cDNA clone
 DEFINITION IMAGE:1222790 3' similar to gb:D42040 RING3 PROTEIN (HUMAN);, mRNA
 sequence.
 ACCESSION A1594823
 VERSION A1594823.1 GI:4603871
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 76)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mousseest@wustl.edu
 This clone is available royalty-free through LNL; contact the

IMAGE Consortium (infoimage.lnlnl.gov) for further information.
 MGI:648382
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Trace considered overall poor quality
 High quality sequence stop: 1.
 Location/Qualifiers

1. 76
 /organism="Mus musculus"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:1222790"
 /clone_id="Stratagene mouse heart (#937316)"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: heart; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTTCTTTT 3'"
 BASE COUNT 12 a 27 c 16 g 21 t
 ORIGIN

Query Match 54.1%; Score 14.6; DB 9; Length 76;
 Best Local Similarity 81.0%; Pred. No. 2.3e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 6 CTTTGAGCCTCAGGCTGAG 26
 ||||| ||||| |||||
 Db 49 CTTTGAGCCTCAGGCTGAG 69

RESULT 12
 N72966 87 bp mRNA linear EST 28-JAN-1997
 LOCUS YV48h11.r1 Soares fetal liver spleen INFPS Homo sapiens cDNA clone
 DEFINITION IMAGE:246021 5' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION N72966
 VERSION N72966.1 GI:1230070
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 87)
 Hillier, L., Lennon, G., Becker, M., Bonaldi, M.F., Chapell, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaekis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 Contact: Wilson R
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.lnlnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 1533 Std Error: 0.00
 Seq primer: reverse ET
 High quality sequence stop: 1.
 Location/Qualifiers

1. 87
 /organism="Homo sapiens"
 FEATURES source

BASE COUNT	ORIGIN	14 a	37 c	25 g	17 t
Query Match	54.1% Score 14.6; DB: 17; Length 93;				
Best Local Similarity	81.0%; Pred. No. 2.5e+04;				
Matches	17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
OY	4 GACTTGGACCTCAGGCTCTG 24				
Db	43 GACCTTGACGCCGCTGCTCTG 63				
RESULT 14					
W82482/c					
LOCUS					
DEFINITION	W82482 m104d03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone	97 bp	mrna	linear	EST 12-SEP-1996
ACCESSION	W82482				
VERSION	W82482.1				
KEYWORDS	EST.				
ORGANISM	house mouse.				
REFERENCE	1 (bases 1 to 97)				
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schenkelberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Watson,R., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Watson,R.				
TITLE	The Maspur-HMT Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M/Mouse EST Project Washu-HMT Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:247837 Trace considered overall poor quality Possible reversed clone; similarity on wrong strand Seq primer: -28M13 rev2 from Amer sham High quality sequence stop: 1. Location/Qualifiers 1..97 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:404069" /clone_1lb="Soares mouse p3NMF19.5" /dev_stage="19.5 dpc total fetus" /lab_host="DH10B (ampicillin resistant)" /note="Vector: pT73D (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer; 15', 7GTTTCCACATCGAAGTGGAGGCGGCGGCAATTTTTTTTTTTT 3', 7GTTTCCACATCGAAGTGGAGGCGGCGGCAATTTTTTTTTTTT 3', digested with Not I and Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73D vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."				
BASE COUNT	32 a	31 c	22 g	12 t	

Query Match 54.1%; Score 14.6; DB 14; Length 97;
 Best Local Similarity 81.0%; Pred. No. 2.5e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 GACTTGAGCTCAGGCTCG 24
 1 ||||| ||||| ||||
 Db 67 GCTTTGACACTCAGCTCTG 47

RESULT 15

AI215770

LOCUS

58 bp

mRNA

linear

EST 02-DEC-1998

DEFINITION

qm39c08.x1 NCI_CGAP_Lu5 Homo sapiens CDNA clone IMAGE:1884206 3'
 similar to SW:POR2_HUMAN P45880 VOLTAGE-DEPENDENT ANION-SELECTIVE
 CHANNEL PROTEIN 2; contains element MER35 repetitive element;;
 mRNA sequence.

ACCESSION

AI215770.1 GI:3784811

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 58)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/dbtp/image/image.html

www.bio.llnl.gov/dbtp/image/image.html

www.bio.llnl.gov/dbtp/image/image.html

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www.bio.llnl.gov/dbtp/image/image.html

www.bio.llnl.gov/dbtp/image/image.html

Search completed: December 21, 2002, 19:26:00
 Job time : 843.041 secs

Query Match

53.3%; Score 14.4; DB 9; Length 58;

Best Local Similarity

93.8%; Pred. No. 2.4e+04;

Matches

15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GCCTCAGGCTCTGAGT 27

Db 13 GCCTCAGGCTCTGAGT 28

BASE COUNT 15 a 15 c 13 g 15 t
 ORIGIN

FEATURES

Trace considered overall poor quality
 Insert length: 1424 Std Error: 0.00
 Seq primer: -40UP from GIBCO
 High quality sequence stop: 1.
 Location/Qualifiers

1..58

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1884206"

/clone_lib="NCI_CGAP_Lu5"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from a

neuroendocrine lung carcinoid, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated

to Eco RI adaptors (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pRT3 vector. Library is normalized. Library was

constructed by Bento Soares and M. Fatima Bonaldo."

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 832.041 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 27

Sequence: 1 UCUGACUUGAGCCUCAGGUCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em.estha:*
2: em.esthum:*
3: em.estin:*
4: em.estnu:*
5: em.estov:*
6: em.estpl:*
7: em.estro:*
8: em.estc:*
9: gb.est1:*
10: gb.est2:*
11: gb.est3:*
12: gb.est4:*
13: gb.est5:*
14: gb.estfun:*
15: em.estom:*
16: em.estom:*
17: gb.gss:*
18: em.gss.hum:*
19: em.gss.inv:*
20: em.gss.pln:*
21: em.gss.vrt:*
22: em.gss.fun:*
23: em.gss.mam:*
24: em.gss.mus:*
25: em.gss.other:*
26: em.gss.pro:*
27: em.gss.tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	59.3	59	17	AZ800849
2	16	59.3	100	10	BE587181
3	15.6	57.8	72	17	FR0010427
4	15.6	57.8	97	12	BG535415
5	15.4	57.0	52	17	AZ597394
6	15.2	56.3	97	9	AA973016

C	7	15.2	56.3	98	14	BO566275	BO566275
C	8	15	55.6	61	17	AZ781308	AZ781308
C	9	14.8	54.8	83	12	BF581859	BF581859
C	10	14.8	54.8	86	9	AA485016	AA485016
C	11	14.6	54.1	79	9	A1594823	A1594823
C	12	14.6	54.1	87	14	N72966	N72966
C	13	14.6	54.1	93	17	BH229029	BH229029
C	14	14.6	54.1	97	14	W82482	W82482
C	15	14.4	53.3	58	9	A1215770	A1215770
C	16	14.4	53.3	62	17	AZ655830	AZ655830
C	17	14.4	53.3	66	17	AZ424287	AZ424287
C	18	14.4	53.3	66	17	AZ602165	AZ602165
C	19	14.4	53.3	70	9	A1000791	A1000791
C	20	14.4	53.3	77	14	D19088	D19088
C	21	14.4	53.3	84	9	AA535865	AA535865
C	22	14.4	53.3	85	10	AA013285	AA013285
C	23	14.4	53.3	85	10	AA089043	AA089043
C	24	14.4	53.3	93	9	AA037489	AA037489
C	25	14.4	53.3	96	13	BI787905	BI787905
C	26	14.4	53.3	97	9	A0259143	A0259143
C	27	14.2	52.6	43	9	AA604155	AA604155
C	28	14.2	52.6	66	17	AZ665590	AZ665590
C	29	14.2	52.6	76	17	AZ789070	AZ789070
C	30	14.2	52.6	77	17	AZ508174	AZ508174
C	31	14.2	52.6	83	17	AZ777224	AZ777224
C	32	14.2	52.6	85	17	AZ944510	AZ944510
C	33	14.2	52.6	88	9	A1937691	A1937691
C	34	14.2	52.6	88	9	AL645462	AL645462
C	35	14.2	52.6	88	17	AZ461077	AZ461077
C	36	14.2	52.6	94	17	AZ812511	AZ812511
C	37	14.2	52.6	96	9	AA880881	AA880881
C	38	14.2	52.6	98	17	AZ481031	AZ481031
C	39	14.2	52.6	100	12	BF944293	BF944293
C	40	14.2	52.6	24	17	AZ807619	AZ807619
C	41	14	51.9	50	9	AU106947	AU106947
C	42	14	51.9	96	14	W76234	W76234
C	43	14	51.9	100	9	AA544623	AA544623
C	44	13.8	51.1	38	17	AZ806846	AZ806846
C	45	13.8	51.1	48	17	AZ514368	AZ514368

ALIGNMENTS

RESULT 1	AZ800849	59 bp	DNA	linear	GSS 16-FEB-2001
DEFINITION	2M0059002F Mouse 10kb plasmid UGCIM library Mus musculus genomic clone UGC2M0059002 F, DNA sequence.				
ACCESSION	AZ800849				
VERSION	AZ800849.1	GI:12953172			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Dunn,D., Moyagi,A., Barber,M., Beacon,T., Duval,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dduenne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00				

Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 3 UGACUUGAGCCUCCAGGUCUG 24
 :||||:|||||:|||||
 Db 39 TGACTTTCAGCCCTGGGTGCG 60

RESULT 4
 BG535415 97 bp mRNA linear EST 03-APR-2001
 LOCUS 602563077F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4687962 5',
 DEFINITION mRNA sequence.
 ACCESSION BG535415
 VERSION BG535415.1 GI:13526960
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 97)
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs.femail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.lnl.gov
 Plate: LNCMI501 row: 1 column: 19
 High quality sequence stop: 97.
 Location/Qualifiers

FEATURES
 source
 1..97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4687962"
 /clone_id="NIH_MGC_77"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
 SfiI (ggccgctggcgc); Site:2: SfiI (ggccattggcgc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGGCCATTATGACC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCAGCGCGCCGACATG-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

BASE COUNT 14 a 26 c 46 g 11 t
 ORIGIN

Query Match 57.8%; Score 15.6; DB 12; Length 97;
 Best Local Similarity 63.6%; Pred. No. 9.1e+03;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 UGACUUGAGCCUCCAGGUC 22
 :||||:|||||:|||||
 Db 64 TCGACTTTCAGCCCTGGGTGCG 43

RESULT 5
 AZ597394 52 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0411B23F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 DEFINITION IMAGE:1577884 3' similar to SW-TCF2_HUMAN P40227 T-COMPLEX PROTEIN
 ACCESSION AZ597394
 VERSION AZ597394.1 GI:11719584
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 1 (bases 1 to 52)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah
 Rm 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0411 row: B column: 23
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 52.
 Location/Qualifiers

FEATURES
 source

1..52
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0411B23"
 /clone_id="Mouse 10kb plasmid UUCG1M library"
 /sex="male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1473211419b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 19 a 8 c 6 g 19 t
 ORIGIN

Query Match 57.0%; Score 15.4; DB 17; Length 52;
 Best Local Similarity 58.8%; Pred. No. 8.4e+03;
 Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 UGACUUGAGCCUCC 17
 :||||:|||||:|||||
 Db 10 TCGACTTTCAGCCCTCA 26

RESULT 6
 AA973016 97 bp mRNA linear EST 20-MAY-1998
 LOCUS op25e03.81 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone
 DEFINITION IMAGE:1577884 3' similar to SW-TCF2_HUMAN P40227 T-COMPLEX PROTEIN
 ACCESSION AA973016
 VERSION AA973016.1 GI:3148196
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 97)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 trace considered overall poor quality
 Seq primer: -40ml3 fwd. EP from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1577884"
 /clone_id="Soares_NFI_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NDH19W, testis NHT, and B-cell
 NCI-CGAP-GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 27 a 26 g 24 t
 ORIGIN
 Query Match 56.3%; Score 15.2; DB 9; Length 97;
 Best Local Similarity 55.0%; Pred. No. 1.4e+04;
 Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 UCUGAGCUCGAGCCGACGAG 20
 :||:|||||:|||||
 Db 8 TCTGGCTTGACCTCAGCG 27

RESULT 7
 BO566275/c 98 bp mRNA linear EST 19-JUN-2002
 LOCUS g156902.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
 DEFINITION BO566275
 VERSION BO566275
 KEYWORDS BO566275.1 GI:21469592
 EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 98)
 AUTHORS Kachar,B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kachar,B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 56 row: 9 column: 02
 Seq primer: M13Rpl reverse primer (ABI).
 Location/Qualifiers

source
 1..98
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g156902"
 /clone_id="Mouse Organ of Corti cDNA pluescript"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /note="Organ: Organ of Corti; Vector: pluescript; The
 organ of Corti (OC) was fine dissected from a total of 386
 OC as follows: 102 samples from post-natal (P) day 5; 72
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
 14 from P12 and 24 from P13. After killing animals by
 cervical dislocation followed by decapitation, the bulla
 was removed and opened in Leibowitz medium. The bony
 capsule of the cochlea was chipped away, stria vascularis
 and spiral ligament were removed and the sensory
 epithelium was carefully dissected out of the modiolus.
 Total RNA was extracted using the micro Fasttrack kit
 (catalog # K1593-02; Invitrogen, Carlsbad, CA), according
 to manufacturer's instructions. Reverse transcription and
 library construction were carried out with the Uni-Zap XR
 vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
 GigaPack III Gold Cloning kit (catalog # 237612), both
 from Stratagene (La Jolla, CA, USA), according to
 manufacturer's instructions. Briefly: 1.5 ug mRNA was
 reverse transcribed using a hybrid oligo(dT) linker-primer
 that contains an Xho I site. First strand synthesis was
 primed with the linker-primer and transcribed using
 Moloney murine leukemia virus reverse transcriptase
 (MMV-RT) and 5-methyl dCTP. The second strand was
 synthesized with DNA polymerase and RNase H. Complementary
 DNA was blunt ended with Pfu DNA polymerase, ligated with
 EcoR I adapters in the presence of ligase and digested
 with Xho I. The cDNA was sequentially size fractionated
 over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
 and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
 columns to enrich for cDNAs greater than 400bp and 1000 bp
 , respectively. The cDNA was then directionally ligated to
 the Uni-Zap XR vector, which had been predigested with
 EcoR I and Xho I. The phagemid was packaged with GigaPack
 III Gold and, upon titration on XL1 Blue MRF' cells, the
 yield of the phage library was estimated to be 11,100,000
 recombinants. Stratagene's EXASist interference
 resistance helper phage (catalogue # 211203) was adopted
 to rescue plasmid DNA from the phages. Upon plating of the
 rescued library, individual cDNA clones were selected and
 grown in 96-well, 2 ml growth plate. Plasmid DNA was
 purified from 200 ul of saturated culture with the
 Concert96(RM) plasmid purification kit (Invitrogen,
 Carlsbad, CA) as instructed by the manufacturer. ESTs from
 the 5' end of the cDNA clones were generated with the
 universal M13 reverse primer (CAGCAAGACGATGACC) and 25%
 strength BigDye terminator sequencing chemistry (Applied
 Biosystems, Foster City, CA). Sequencing reactions were
 performed on MJ Tetrad thermal cyclers (MJ Research,
 Watlham, MA), and analyzed on 3700 automated capillary
 sequencers using POP5 polymer (Applied Biosystems, Foster
 City, CA). The frequency distribution of the library is
 as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
 genes are present in Genbank and have know function; 23%
 have hits in Genbank, but do not have assigned function;
 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 23 a 29 g 26 t
 ORIGIN
 Query Match 56.3%; Score 15.2; DB 14; Length 98;
 Best Local Similarity 55.0%; Pred. No. 1.4e+04;
 Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Oy 8 UUGAGCUCGAGGCGUGAGU 27
 ::|||:|||||:|||||

Dn 94 TTCATCTCAGGTCGAAT 75

RESULT 8
LOCUS A2781308 61 bp DNA linear GSS 16-FEB-2001
DEFINITION 2K0019P04R Mouse 10kb plasmid UNGCIM library Mus musculus genomic clone UNGC2M0019F04 R, DNA sequence.
ACCESSION A2781308
VERSION A2781308.1 GI:12913872
KEYWORDS GS.
SOURCE house mouse,
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 61)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weisls,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0019 row: F column: 04
Seq primer: CACACGAAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 61.

FEATURES
Source location/Qualifiers
1..61
 /organism="Mus musculus"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="UNG2M0019F04"
 /clone_lib="Mouse 10kb plasmid UNGCIM library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMW42 (g14732114blAF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into Chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 6 c 21 g 22 t
ORIGIN
Query Match 55.6%; Score 15; DB 17; Length 61;
Best Local Similarity 52.28; Pred. No. 14e+04;
Matches 12; Conservative 6; Mismatches 5; Indels 0; Gaps 0
:::|||||::|| ::|||::|:

Db	6	TCTGACGTGAGATCAGGCTCT	28	
RESULT 9				
BF581859/c			83 bp	mRNA
LOCUS	602099323F1	NCI_CGAP_Co24	Mus musculus	cDNA clone IMAGE:4219204 5',
DEFINITION	mRNA sequence.			
ACCESSION	BF581859			
VERSION	BF581859.1	GI:11655675		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	1 (bases 1 to 83)			
JOURNAL	NIH-MGC http://www.ncbi.nlm.nih.gov/			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: Jeffrey E. Green, M.D.			
	cDNA Library Preparation: Life Technologies, Inc.			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	plate: LHAM9800 row: n column: 05			
	High quality sequence stop: 83.			
FEATURES	Location/Qualifiers			
source	1..83			
	/organism="Mus musculus"			
	/strain="FVB/N"			
	/db_xref="taxon:10090"			
	/clone_image="4219204"			
	/clone_lib="NCI_CGAP_Co24"			
	/lab_host="DH10B (TI phage-resistant)"			
	/note="Organ: colon; Vector: PCMV-SPOrt6; Site:1: NotI;			
	Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.			
	Average insert size 1.6 kb. Constructed by Life			
	Technologies. Note: this is a NCI_CGAP Library."			
BASE COUNT	24 a	26 c	19 g	14 t
ORIGIN				
Query Match	54.8%	Score 14.8;	DB 12;	Length 83;
Best Local Similarity	57.7%;	Pred No.1,9e+04;		
Matches 15;	Conservative 4;	Mismatches 7;	Indels 0;	Gaps 0
QY	1	UCGACUUGAGCCUCCAGGCTCAG	26	
Db	42	TCTGCGAGGATCTATGCGCTG	17	
RESULT 10				
AA485016/c			89 bp	mRNA
LOCUS	a439f08.r1	NCI_CGAP_GCB1	Homo sapiens	cDNA clone IMAGE:815655 5',
DEFINITION	mRNA sequence.			
ACCESSION	AA485016			
VERSION	AA485016.1	GI:2214235		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 89)			
	NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			

Tissue Procurement: Louis M. Staedt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldi, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 73.
 Location/Qualifiers

FEATURES

source

1. 89
 /organism="Homo sapiens"
 /db_xref="GDB:6035132"
 /db_xref="taxon:9606"
 /clone="IMAGE:815655"
 /clone_lib="NCI-CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, 19D-), provided by Dr. Louis M. Staedt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
 5'-TGTTACCATCTGATGAGGAGGCGGCGCTCTTTTCTTTTCTTTT-3'
 }. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldi."
 BASE COUNT 27 a 24 c 22 g 16 t
 ORIGIN

Query Match 54.8%; Score 14.8; DB 9; Length 89;
 Best Local Similarity 61.1%; Pred. No. 2e+04;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Oy 7 UUGAGCCUCAGGUCUG 24
 ::::||||| ||| ||| :
 Db 61 TTGAGCCGACAGTGTCTG 44

RESULT 11

A1594823

LOCUS 76 bp mRNA linear EST 21-Apr-1999
 DEFINITION vv18e08.x1 Stragatene mouse heart (#937316) Mus musculus CDNA clone
 IMAGE:1222790 3' similar to gb:D42040 RIN03 PROTEIN (HUMAN);, mRNA
 sequence.

ACCESSION A1594823.1 GI:4603871
 VERSION A1594823
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 76)
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathia: Muridae: Murinae: Mus.
 Marti, M., Hillier, L., Kucaba, T., Martin, D., Beck, C., Wylie, T., Underwood, K., Stephens, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shio, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
 The WashU-NCI Mouse EST Project 1999

TITLE Unpublished (1999)
 JOURNAL Contact: Maria M/WashU-NCI Mouse EST Project 1999
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:648382
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Trace considered overall poor quality
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1. 76
 /organism="Mus musculus"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone="IMAGE:1222790"
 /clone_lib="Stratagene mouse heart (#937316)"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: heart; Vector: phagescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAAATCGCAGAG 3' -3' adaptor sequence: 5' CTGAGCTTTTCTTTTCTTTT 3'."
 BASE COUNT 12 a 27 c 16 g 21 t
 ORIGIN

Query Match 54.1%; Score 14.6; DB 9; Length 76;
 Best Local Similarity 52.4%; Pred. No. 2.3e+04;
 Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Oy 6 CUUGAGCCUCAGGUCUG 26
 :::: ||: ||| ||| :
 Db 49 CTTCCTCTCAGAGTGTGAG 69

RESULT 12

N72966

LOCUS 87 bp mRNA linear EST 28-JAN-1997
 DEFINITION vv48h11.f1 Soares fetal liver spleen JNPLS Homo sapiens CDNA clone
 IMAGE:246021 5' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN)
 sequence.

ACCESSION N72966.1 GI:1230070
 VERSION N72966
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 87)
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chappell, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rinkin, L., Rohlfing, T., Schellendberg, K., Soares, J.B., Tan, F., Thierrey-Meg, J., Trevas, E., Underwood, K., Wolldmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478

TITLE Contact: Wilson RK
 JOURNAL Washington University School of Medicine
 MEDLINE 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 97044478
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1533 Std Error: 0.00
 Seq primer: reverse ET
 High quality sequence stop: 1.

FEATURES
 source
 1. 87
 /organism="Homo sapiens"

Query Match	54.1%;	Score 14.6;	DB 14;	Length 87;	
Best Local Similarity	56.5%;	Pred. No. 2.4e+04;			
Matches 13;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;	
Oy	4	GACUUGAGCCGACGAGUCUGAG	26		
Db	47	GACNNCTACCTCCAGAGTGAG	25		
RESULT 13					
LOCUS	BH229029	93 bp	DNA	linear	GSS 08-NOV-2001
DEFINITION	1006149603.2EL.y1 1006 - Rescuemu Grid G Zea mays genomic, DNA				
ACCESSION	BE229029				
VERSION	BH229029.1	GI:16830667			
KEYWORDS	GSS.				
SOURCE	Zea mays.				
ORGANISM	Zea mays				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC				
	Clade: Panicoideae; Andropogoneae; Zea.				
	1 (bases 1 to 93)				
REFERENCE	Walbot,V.				
AUTHORS	Maize genomic sequences found using engineered Rescuemu transposon				
TITLE	Unpublished (2001)				
JOURNAL	Contact: Walbot V				
COMMENT	Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 106149 row: 10 Class: transposon-tagged. Location/Qualifiers 1..93 /organism="Zea mays" /cultivar="mixed background W23/A186/B73" /db_xref="taxon:4577" /clone_lib="1006 - Rescuemu Grid G" /tissue_type="leaf" /dev_stage="adult" /lab_host="PH10B" /note="Organ: leaf; Vector: Rescuemu (engineered from plasmid pBlueScript backbone); Site.1: BamHI; Site.2: BglII; Rescuemu is a 4.9 kb, modified rescue from total genomic DNA, designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu and follow the links for 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was				

BASE COUNT	ORIGIN	14 a	37 c	25 g	17 t
Query Match	54.1% Score 14.6; DB: 17; Length 93;				
Best Local Similarity	61.9%; Pred. No. 2.5e+04;				
Matches 13; Conservative	4; Mismatches 4; Indels 0; Gaps 0;				
OY	4 GACUUGAGCCCTCAGGCTCUG 24				
Db	43 GACGTTGAGCCGCTGCTGTG 63				
RESULT 14					
W82482/c					
LOCUS					
DEFINITION	W82482. 97 bp mRNA linear EST 12-SEP-1996				
ACCESSION	M040403.r1 Soares mouse p1NMF19.5 Mus musculus cDNA clone				
VERSION	IMAG:404069 5' similar to PIR:A56059 A56059				
KEYWORDS	protein-tyrosine-phosphatase ;, mRNA sequence.				
SOURCE	W82482.1 GI:1393436				
ORGANISM	EST house mouse.				
REFERENCE	Mus musculus				
AUTHORS	Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus. 1 (bases 1 to 97)				
	Geisel, S., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,				
	Marrs, M., Knudsen, T., Lacy, M., Le, M., Martin, J., Morris, M.,				
	Schellingberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,				
	Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and				
	Waterston, R.				
	The WashU-HHMI Mouse EST Project				
	Unpublished (1996)				
	Contact: Maria M/Mouse EST Project				
	WashU-HHMI Mouse EST Project				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
	Tel: 314 286 1800				
	Fax: 314 286 1810				
	Email: mouseest@watson.wustl.edu				
	This clone is available royalty-free through LNL; contact the				
	IMAG Consortium (info@image.lnl.gov) for further information.				
	MCI:247837				
	Traces considered overall poor quality				
	Possible reversed clone; similarity on wrong strand				
	Seq primer: 28M13 rev2 from Amersham				
	High quality sequence stop: 1.				
FEATURES					
SOURCE					
	1..97				
	/organism="Mus musculus"				
	/db_xref="taxon:10090"				
	/clone="IMAGE:404069"				
	/clone.lib="Soares mouse p1NMF19.5"				
	/dev_stage="19.5 dpc total fetus"				
	/lab_host="DH10B (ampicillin resistant)"				
	/note="Vector: pUT3D (Pharmacia) with a modified				
	polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA				
	template: Site:1: Not I; Site:2: Eco RI; 1st strand cDNA				
	double-stranded cDNA was size selected, ligated to Eco RI				
	adapters (Pharmacia), digested with Not I and cloned into				
	the Not I and Eco RI sites of a modified pUT3 vector				
	(Pharmacia). Library went through one round of				
	normalization to a Cot=5 library constructed by Bento				
	Soares and M.Fatima Bonaldo. RNA was kindly provided by				
	Dr. Minoru Ko (Wayne State University)."				

Query Match	54.1%	Score 14.6;	DB 14;	Length 97;
Best Local Similarity	52.4%;	Pred. No. 2.5e+04;		
Matches 11; Conservative	6;	Mismatches 4;	Indels 0;	Gaps 0;

QY 4 GACUUGAGCCUCAGGGUCUG 24
| | : : | | : | | : | : |
Db 67 GTCCTTGAACTCAAGTCTCTG 47

RESULT 15	LOCUS	DEFINITION
AI215770	58 bp mRNA	linear EST 02-DEC-1998
qmq39gc08.x1	NCI-CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1884206 3'	

ACCESSION	AI215770
VERSION	AI215770.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (pages 1 to 58)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Trace considered overall poor quality
Insert Length: 1424 Std Error: 0.00
Seq primer: -400P from G1bco
High quality sequence stop: 1.

FEATURES	Location/Qualifiers
source	1. .58

```

15  /lab_host="DH103"
16  /note="Organ: Lung; Vector: p773D-Pac (Pharmacia) with a
17  modified polylinker; 1st strand cDNA was prepared from
18  neuroendocrine lung carcinoma, and was then primed with a
19  Not I - oligo(dT) primer. Double-stranded cDNA was ligated
20  to Eco RI adaptors (Pharmacia), digested with Not I and
21  cloned into the Not I and Eco RI sites of the modified
22  p773 vector. Library is normalized. Library was
23  constructed by Bento Soares and M. Fatima Bernaldo. "
24

```

Query Match	53.3%;	Score 14.4;	DB 9;	Length 58;
Best Local Similarity	68.8%;	Pred. No. 2.4e+04;		
Matches	11;	Conservative	4;	Mismatches 1;
				Indels 0;
				Gaps 0;

Qy	12	GCCTCAGGCTCAGAGT	27
Db	13	GCCTCAGAGTCTGAGT	28

Search completed: December 21, 2002, 19:26:01
Job time : 833.041 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 554.694 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-26
Perfect score: 18
Sequence: 1 GGATTCATCGAGCGATCG 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estic:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estin:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	73.3	86	17	BH629707 100707580
2	13.2	73.3	87	14	BQ239833 1A605026D
3	12.8	71.1	53	17	AL769486 1A769486
4	12.8	71.1	60	14	BQ757618 EBem10_SQ
5	12.8	71.1	74	10	AV565503 1A769486
6	12.8	71.1	80	17	AZ661791 1M0540J04

Result No.	Score	Query Match	Length	ID	Description
7	12.8	71.1	81	14	BQ757211 EBem10_SQ
8	12.8	71.1	93	17	AA736573 0A18C05_S
9	12.8	71.1	94	17	BH811235 5A1K_0578
10	12.8	71.1	97	12	BG778506 60266719
11	12.8	71.1	98	17	AZ606926 1M0429A10
12	12.8	71.1	98	17	AL761738 1A761738
13	12.8	71.1	98	12	BG778436 60266627
14	12.8	71.1	80	17	AZ784908 2M0028F18
15	12.2	67.8	37	17	AZ833759 2M0116M01
16	12.2	67.8	48	17	AZ805363 1M0097H13
17	12.2	67.8	61	17	AZ356616 1M0097H13
18	12.2	67.8	46	9	AI155176 1A155176
19	11.8	65.6	38	17	AZ581309 1M0370E06
20	11.8	65.6	31	17	AZ447531 1M0244C15
21	11.8	65.6	51	17	B06639 1A089435
22	11.8	65.6	61	14	W48103 1A48103
23	11.8	65.6	68	17	AZ492365 1M0326023
24	11.8	65.6	73	17	AZ694238 1A769486
25	11.8	65.6	75	17	BH806709 1M0807580
26	11.8	65.6	78	9	AA786689 1A786689
27	11.8	65.6	85	9	AI462362 1A462362
28	11.8	65.6	86	17	AZ485774 1A485774
29	11.8	65.6	86	17	BQ56702 1A56702
30	11.8	65.6	95	9	AF21606 1A21606
31	11.8	65.6	100	9	AA089435 1A089435
32	11.8	65.6	100	14	BQ846904 1A846904
33	11.8	64.4	30	17	BH814304 1A814304
34	11.6	64.4	30	17	TA131A020 1A131A020
35	11.6	64.4	43	9	AI492250 1A492250
36	11.6	64.4	62	17	AZ608873 1A608873
37	11.6	64.4	67	13	BM021089 1A021089
38	11.6	64.4	67	13	BM021128 1A021128
39	11.6	64.4	68	13	BI966026 1A966026
40	11.6	64.4	68	13	BM126239 1A126239
41	11.6	64.4	68	17	AZ772124 1A772124
42	11.6	64.4	69	9	AA168290 1A168290
43	11.6	64.4	77	14	BQ761092 1A761092
44	11.6	64.4	81	17	AZ498215 1A498215
45	11.6	64.4	82	17	AZ657340 1A657340

ALIGNMENTS

RESULT 1
LOCUS BH629707/c 86 bp DNA linear GSS 30-JAN-2002
DEFINITION 1007075806.2EL_x1 1007 - Rescueru Grid H Zea mays genomic. DNA
ACCESSION BH629707
VERSION BH629707.1 GI:18442958
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
JOURNAL clade; Panicoideae; Andropogoneae; Zea.
COMMENT 1 (bases 1 to 86)
Walbot, V.
Maize genomic sequences found using engineered Rescueru transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007075 column: 36
Class: transposon-tagged
Location/Qualifiers

FEATURES

source

1..86
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1007 - Rescuenmu Grid H"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescuenmu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; Rescuenmu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuenmu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuenmu'. Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 35 c 23 g 17 t

ORIGIN

Query Match 73.3%; Score 13.2; DB 17; Length 86;
Best Local Similarity 83.3%; Pred. No. 8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATGG 18
||||| |||||||||

Db 52 GGAAGATTCGAGCGATGG 35

RESULT 2
BQ239833/c 87 bp mRNA linear EST 03-MAY-2002
LOCUS TAE05026D02R TAE05 Triticum aestivum CDNA clone TAE05026D02R, mRNA
DEFINITION
BQ239833 sequence.
ACCESSION BQ239833
VERSION BQ239833.1 GI:20435696
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticaceae; Triticum.
1 (bases 1 to 87)
REFERENCE Cloutier, S.
AUTHORS Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-Food Canada
195 Datoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 026 row: D column: 02
Seq primer: M13 Reverse.

FEATURES
source
1..87
Location/Qualifiers
/organism="Triticum aestivum"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone_lib="TAE05026D02R"
/clone_1ib="TAE05"
/tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 5 days post-anthesis"

BASE COUNT 7 a 44 c 23 g 13 t

ORIGIN

Query Match 73.3%; Score 13.2; DB 14; Length 87;
Best Local Similarity 83.3%; Pred. No. 8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATGG 18
||||| |||||||

Db 66 GGAATCGTCGAGCGATGG 49

RESULT 3
AL769486/c 53 bp DNA linear GSS 19-JUN-2002
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-086G01-012541, genomic survey sequence.
ACCESSION AL769486
VERSION AL769486.1 GI:21531688
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weissshaar, B.
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
Unpublished

REFERENCE 2
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 53)
Li, Y., Strizhov, N., Rosso, M. and Weissshaar, B.
Direct Submission
Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the right border of the T-DNA. It indicates an insertion within the locus defined by clone f15h18.
The sequences are generated at the MPI for Plant Breeding Research German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
1..53
Location/Qualifiers
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GK-086G01-012541"
/clone_1ib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 13 a 14 c 19 g 7 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 17; Length 53;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCGATGG 18

Db 23 ACTCATCGAGCGCTGG 8

RESULT 4
B0757618/c
LOCUS
DEFINITION
B0757618 60 bp mRNA linear EST 26-JUL-2002
Ebm10_S0004.L03_R embryo, 2 day germination, no treatment, cv
Optic, Ebem10 Hordeum vulgare cDNA clone Ebem10_S0004.L03 5', mRNA
sequence.

ACCESSION
B0757618
VERSION
B0757618.1 GI:21966090
KEYWORDS
EST.
SOURCE
Hordeum vulgare.
ORGANISM
Hordeum vulgare.
REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Trilicaceae; Hordeum.
1 (bases 1 to 60)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scrl.sarl.ac.uk.
Location/Qualifiers

FEATURES
source
1..60
/organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
/clone="Ebem10_S0004.L03"
/clone_lib="embryo, 2 day germination, no treatment, cv
Optic, Ebem10"
/tissue_type="embryo"
/dev_stage="2 day germination"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from embryos dissected from germinating grains (2
day) in glasshouse grown barley plants. Developed as part
of the barley transcriptome resources of BBSRC/SERAD
funded cereal iGF (Investigating Gene Function) project."

BASE COUNT
10 a 23 c 22 g 5 t

ORIGIN
Query Match 71.1%; Score 12.8; DB 14; Length 60;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCGATGG 18
Db 50 ACTCATCGAGCGATGG 35

RESULT 5
AV565503/c
LOCUS
DEFINITION
AV565503 74 bp mRNA linear EST 07-SEP-2000
Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone SQ25d12f 3', mRNA sequence.

ACCESSION
AV565503
VERSION
AV565503.1 GI:8736945
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 74)

REFERENCE
1 (bases 1 to 74)

AUTHORS
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)

JOURNAL
MEDLINE
20363093
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yama 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp; URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
source
1..74
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ25d12f"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT
26 a 13 c 11 g 24 t

ORIGIN
Query Match 71.1%; Score 12.8; DB 10; Length 74;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAATCATCGAGCGATG 17
Db 36 GAATCATCGAGCGATG 21

RESULT 6
AZ661791/c
LOCUS
DEFINITION
AZ661791 80 bp DNA linear GSS 14-DEC-2000
clone U06C1M0540J04 R, DNA sequence.

ACCESSION
AZ661791
VERSION
AZ661791.1 GI:11798937
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 80)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weils, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weils
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 565 5606
Fax: 801 385 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0540 row: J column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 80.
Location/Qualifiers

FEATURES
source
1..80
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0540J04"
/clone_lib="Mouse 10kb plasmid U06C1M library"


```

OY      2  GAATCATCGAGCATG 17
      11 | | | | | | | | | |
Db      39  GAGCCATCGAGCATG 24

RESULT 9
LOCUS   BH811235
DEFINITION 94 bp DNA linear GSS 02-MAY-2002
          SALK_057886 Arabidopsis thaliana TDNA insertion lines Arabidopsis
          thaliana genomic clone SALK_057886, DNA sequence.
ACCESSION  BH811235
VERSION    BH811235.1 GI:20389177
KEYWORDS  GSS.
SOURCE    thale cress.
ORGANISM  Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
AUTHORS   , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
          Zimmerman,J. and Ecker,J.R.
          A Sequence-Indexed Library of Insertion Mutations in the
          Arabidopsis Genome
          Unpublished (2001)
JOURNAL   Salk Institute Genomic Analysis Laboratory (SIGAL)
COMMENT    The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Fax: 858 558 6379
          Email: eckersalk.salk.edu
          This is single pass sequence recovered from the left border of
          TDNA. This sequence lies within an annotated exon of Atlg69400.
          Class: TDNA tagged.
          Location/Qualifiers
            1..94
            /organism="Arabidopsis thaliana"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone_lib="SALK_057886"
            /note="PCR was performed on Arabidopsis thaliana lines"
            /note="each of which contains one or more TDNA insertion"
            /note="elements. The resultant fragment for each line was"
            /note="directly sequenced to determine the genomic sequence at"
            /note="the site of insertion. Details of the protocols used can"
            /note="be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT  26 a 16 c 23 g 29 t

ORIGIN
Query Match 71.1%; Score 12.8; DB 17; Length 94;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1  GGAATCATCGAGCAT 16
      11 | | | | | | | | | |
Db      49  GGACTCATCGATCAT 64

RESULT 10
LOCUS   BG778506
DEFINITION 97 bp mRNA linear EST 15-MAY-2001
          60266719F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4806509 5',
          mRNA sequence.
ACCESSION  BG778506
VERSION    BG778506.1 GI:14048823
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  1 (bases 1 to 97)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
          Email: cgabs-remail.nih.gov
          Tissue Procurement: DCTD/DRP
          cDNA Library Preparation: CLONTECH Laboratories, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LMNL at:
          http://image.llnl.gov
          Plate: DCCM1656 Row: e Column: 06
          High quality sequence start: 6
          High quality sequence stop: 97.
          Location/Qualifiers
            1..97
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_image="IMAGE:4806509"
            /clone_lib="NIH_MGC_60"
            /issue_type="adenocarcinoma"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
            Site 1: SfiI (ggcgccgcgcgc); Site 2: SfiI (ggcattatggcc
            5'; and 3' adaptors were used in cloning as follows: 5'
            adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCCAGCATC-AT(30)BA-3'
            (where B = A, C, or G and N = A, C, G, or T). Average
            insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
            contained inserts by PCR. This library was enriched for
            full-length clones and was constructed by Clontech
            Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
            Library."

BASE COUNT  17 a 21 c 24 g 35 t

ORIGIN
Query Match 71.1%; Score 12.8; DB 12; Length 97;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      3  AATCATCGAGCATG 18
      11 | | | | | | | | | |
Db      68  AATCAACGAGCATG 53

RESULT 11
LOCUS   AZ606926
DEFINITION 98 bp DNA linear GSS 13-DEC-2000
          IM0429A10F Mouse 10kb plasmid U06C1M library Mus musculus genomic
          clone U06C1M0429A10 F, DNA sequence.
ACCESSION  AZ606926
VERSION    AZ606926.1 GI:11729116
KEYWORDS  GSS.
SOURCE    house mouse.
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 98)
          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly
          ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
          and Wright,D., Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
          Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA

```


/tissue_type="adenocarcinoma"
 /lab_host="DHI0B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggcccttcggcc); Site_2: SfiI (ggcccttcggcc
); Double-stranded cDNA was prepared from cell 11e RNA.
 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTTAGGCG-3' and 3' adaptor
 sequence: 5'-ATCTAGAGCGCGAGCGCGGCACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
 library."

BASE COUNT 17 a 23 c 25 g 34 t
 ORIGIN
 Query Match 71.1%; Score 12.8; DB 12; Length 99;
 Best Local Similarity 87.5%; Pred. No. 1.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATGAGCGCATG 18
 ||||| |||||
 Db 68 AATCAGCCAGCATG 53
 RESULT 14
 AZ784908 80 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0028F18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0028F18 F, DNA sequence.
 ACCESSION AZ784908
 VERSION AZ784908.1 GI:12921118
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota: Metazoa; Chordata: Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 80)

TITLE
 JOURNAL
 COMMENT
 Durr, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: F column: 18
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 80.

FEATURES

1. 80 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0028F18"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 digested DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (911473211491AT12072.1), a copy number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 19 a 16 c 27 g 18 t
 ORIGIN
 Query Match 68.9%; Score 12.4; DB 17; Length 80;
 Best Local Similarity 92.9%; Pred. No. 2e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AATCATGAGCGCAT 16
 ||||| |||||
 Db 80 AATCATTGAGCAT 67
 RESULT 15
 AZ833759 37 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0116M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0116M01 F, DNA sequence.
 ACCESSION AZ833759
 VERSION AZ833759.1 GI:13003667
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota: Metazoa; Chordata: Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 37)

TITLE
 JOURNAL
 COMMENT
 Durr, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0116 row: M column: 01
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 37.

FEATURES

1. 37 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0116M01"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 9 a 4 c 12 g 12 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 17; Length 37;
Best Local Similarity 82.4%; Pred. NO. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAATCATCGAGGCATGG 18
||||| |||||||
DB 3 GAATCATCGAGGCATGG 19

Search completed: December 21, 2002, 19:26:11
Job time : 564.694 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 801.224 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-27

Sequence: 26
1 CACTGACCACTGATTTAAGCAGAG 26

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_rtl:*
22: em_gss_fun:*
23: em_gss_hum:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	75	14	H55528
2	17	65.4	97	9	AA282576
3	16.4	63.1	92	14	H55144
4	15.2	58.5	92	9	AA460218
5	15	57.7	93	12	BP434056
6	14.8	56.9	82	17	AZ454421

Result No.	Score	Query Match	Length	DB ID	Description
7	14.6	56.2	91	17	BP790845
8	14.4	55.4	24	17	AZ866592
9	14.4	55.4	40	9	AU011413
10	14.4	55.4	84	17	AZ918464
11	14.4	55.4	91	17	AA721220
12	14.4	55.4	100	9	A1536504
13	14.2	54.6	75	12	BG408667
14	14.2	54.6	80	14	H55918
15	14.2	54.6	84	10	AM166739
16	14.2	54.6	88	17	AA780578
17	14.2	54.6	86	17	DR15M4T
18	14.2	53.8	46	9	AV771016
19	14.2	53.8	63	10	AV833914
20	14.2	53.8	64	10	BE638305
21	14.2	53.8	67	9	AA721395
22	14.2	53.8	73	10	AM626539
23	14.2	53.8	84	17	AZ315745
24	14.2	53.8	87	17	AZ243566
25	14.2	53.8	87	17	BG060109
26	14.2	53.8	92	12	BF063884
27	13.8	53.1	74	17	AZ853652
28	13.8	53.1	81	17	BH623969
29	13.8	53.1	86	14	BQ127726
30	13.8	53.1	86	17	AZ789821
31	13.8	53.1	87	13	B1493713
32	13.8	53.1	90	9	A1596246
33	13.8	53.1	98	17	BH866038
34	13.8	53.1	100	10	BE073710
35	13.8	53.1	100	12	BF908892
36	13.6	52.3	47	9	A1813483
37	13.6	52.3	51	9	AA559169
38	13.6	52.3	62	12	BG879275
39	13.6	52.3	62	17	AZ622457
40	13.6	52.3	70	9	AA777046
41	13.6	52.3	73	9	AA509351
42	13.6	52.3	73	9	AA509704
43	13.6	52.3	74	17	AZ658469
44	13.6	52.3	78	9	AA904704
45	13.6	52.3	80	9	AA484332

ALIGNMENTS

RESULT 1
H55528
LOCUS
DEFINITION
H55528
mRNA sequence.
ACCESSION
H55528
VERSION
H55528.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
Trofatter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gussella, J.F. and Buckler, A.J.
An expression-independent catalog of genes from human chromosome 22 (bases 1 to 75)
Mammalian Genome Res. 5 (3), 214-224 (1995)
96159527
COMMENT
Contact: Buckler AJ
Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Tel: 6177249616
Fax: 6177265736
Email: buckler@helix.mgh.harvard.edu
Seq primer: T3.
location/Qualifiers
1..75
/organism="Homo sapiens"

/db_xref="taxon:9606"
 /clone_id="Chromosome 22 exon"
 /lab_host="E. coli DH5a"
 /note="Vector: pBluescriptKS+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptKS+ at the Sal I and Bam HI sites."
 BASE COUNT 17 a 17 c 19 g 22 t
 ORIGIN
 Query Match 100.0%; Score 26; DB 14; Length 75;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CACTCAGCCACTGGATTAAACGAG 26
 |||||||
 DB 45 CACTCAGCCACTGGATTAAACGAG 70
 RESULT 2
 AA282576 97 bp mRNA linear EST 13-AUG-1997
 LOCUS z13c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713004 3',
 mRNA sequence.
 ACCESSION AA282576
 VERSION AA282576.1 GI:1925492
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 97)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 695 Std Error: 0.00
 Seq primer: -41ml3 fwd. ET from Amersham
 High quality sequence stop: 61.
 location/Qualifiers
 1. 97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:713004"
 /clone_lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCATCTGAGTGGAGCGCCCTCATTTTCTTTTCTTTT-3',
 1. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 38 a 13 c 12 g 34 t
 ORIGIN
 Query Match 65.4%; Score 17; DB 9; Length 97;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CACTCAGCCACTGGATTAAACGAG 26
 |||||||
 DB 45 CACTCAGCCACTGGATTAAACGAG 70
 RESULT 2
 AA282576 97 bp mRNA linear EST 13-AUG-1997
 LOCUS z13c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713004 3',
 mRNA sequence.
 ACCESSION AA282576
 VERSION AA282576.1 GI:1925492
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 97)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 695 Std Error: 0.00
 Seq primer: -41ml3 fwd. ET from Amersham
 High quality sequence stop: 61.
 location/Qualifiers
 1. 97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:713004"
 /clone_lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCATCTGAGTGGAGCGCCCTCATTTTCTTTTCTTTT-3',
 1. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 38 a 13 c 12 g 34 t
 ORIGIN

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CACTCAGCCACTGGATTAAACGAG 25
 |||||||
 DB 43 CACTCAGCCACTGGATTAAACGAG 67
 RESULT 3
 H55144/c 92 bp mRNA linear EST 07-DEC-1995
 LOCUS CHR220083 Chromosome 22 exon Homo sapiens cDNA C22.110 5',
 mRNA sequence.
 ACCESSION H55144
 VERSION H55144.1 GI:1108010
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 92)
 AUTHORS Trofatter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F.
 and Buckler, A.J.
 An expression-independent catalog of genes from human chromosome 22
 Genome Res. 5 (3), 214-224 (1995)
 96159527
 COMMENT Contact: Buckler AJ
 Molecular Neurogenetics Unit
 Massachusetts General Hospital
 Building 149, 13th St., Charlestown MA 02129
 Tel: 6177249616
 Fax: 6177265736
 Email: buckler@helix.mgh.harvard.edu
 Seq primer: T3
 location/Qualifiers
 1. 92
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="C22.110"
 /clone_lib="Chromosome 22 exon"
 /lab_host="E. coli DH5a"
 /note="Vector: pBluescriptKS+; Site_1: Sal I; Site_2:
 Bam HI (destroyed); Exons were isolated from human
 chromosome 22 specific cosmids using a modification of
 the method of exon amplification (Proc. Natl. Acad. Sci.
 USA 88:4005-4009, 1991). Amplified exons were digested
 with Sal I and Bgl II and subsequently cloned into
 pBluescriptKS+ at the Sal I and Bam HI sites."
 BASE COUNT 24 a 24 c 28 g 16 t
 ORIGIN
 Query Match 63.1%; Score 16.4; DB 14; Length 92;
 Best Local Similarity 76.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CACTCAGCCACTGGATTAAACGAG 26
 |||||||
 DB 66 CCCTCAGCCCTGGATTATGTGAG 41
 RESULT 4
 AA460218/c 92 bp mRNA linear EST 09-JUN-1997
 LOCUS zx50f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795691
 5', mRNA sequence.
 ACCESSION AA460218
 VERSION AA460218.1 GI:2185034
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 92)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1). The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

	Best Match	56.9%;	Score 14.8;	DB 17;	Length 82;
	Best Local Similarity	73.1%;	Pred. No. 1e+04;		
Matches	19;	Conservative	0;	Mismatches	7;
				Indels	0;
				Gaps	0;
OY	1 CACTCAGCCACTCGATTTAACGACAG	26	.		
Dδ	19 CATTCAGTCACTTGAAAAAACCGAG	44			

Accession	Result 7	91 bp	DNA	linear	GSS 02-APR-2002
BH790845/c					
LOCUS					
DEFINITION					
SALK_058039.54.15.x Arabidopsis thaliana cDNA insertion lines					
Arabidopsis thaliana genomic clone SALK_058039.54.15.x, DNA sequence.					

ACCESSION	BH790845	
VERSION	BH790845.1	GI:198839888
KEYWORDS	GSS,	
SOURCE	thale cress,	
ORGANISM	Arabidopsis thaliana	

ORGANISM
Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 91)

Authors	Title	Journal	Comment
Alonso, J.M., Leisse, T.U., Barajas, P., Chen, H., Kneib, R., Gaarand, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Preudis, L., Shinn, P., Zimmerman, J., and Ecker, J. R.	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome	Unpublished (2001)	Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckere@salk.edu
This is single pass sequence recovered from the left border of
TMDNA. This sequence lies within an annotated exon of
Class: TMDNA tagged.

FEATURES
SOURCE

```

1..91
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_058039.54.15.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can

```

```

be found at http://signal.salk.edu/ttna_protocols.html
BASE COUNT      21 a      24 c      12 g      34 t
ORIGIN

```

Query Match	56.2%;	Score 14.6;	DB 17;	Length 91;
Best Local Similarity	81.0%;	Pred. No. 1.4e+04;		
Matches 17; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

OY 4 TCAGCCACTGGATTTAAGCAG 24
 | | | | | | | | | | | |
 Db 87 TAAGAGACTGGATTTAAGCAG 67

RESULT 8
AZ866692/c
T00TS
X7966603
24 hr
DMM
140000
CCS 21-1111-2001

LOCUS	24 bp
A2600692	
DEFINITION	2M0177F18F Mouse 10kb plasmid UUGC1A
clone UUGC2M0177F18 F, DNA sequence	
UUGC0000	

ACCESSION	AZ866692	GI:13068253
VERSION	AZ866692.1	
KEYWORDS	GSS.	

SOURCE	ORGANISM	house mouse. Mus musculus Eukaryota; M

REFERENCE
AUTHORS
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

TITLE
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rai,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 595 5506

Tel: 801 585 3606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Err

```

insert length: 10000      size error:
Plate: 0177  row: F      column: 18
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends

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	High quality sequence stop: 24.
FEATURES	Location/Qualifiers
source	1. .24

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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```

/clone="UUGC2M01/F18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/ab_heat="904 studies with 613 M. musculus

```

musculus C57BL/6J (male) was obtained from the Jackson Laboratory, Maine, DNA was extracted from the tail

laboratory mouse DNA resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared nu-

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess.

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivativator

of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to adaptor DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells

BASE COUNT 6 a 2 c 9 g 7 t
 and selected for ampicillin resistance."

ORIGIN

Query Match 55.4%; Score 14.4; DB 17; Length 24;
 TITLE
 Best Local Similarity 75.0%; Pred. No. 8.1e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 ACTCAGCAGCTGATTAAGCAGA 25
 ||||| || ||||| |||||
 DB 24 ACTCAGCAGCTCATTTCTCAGA 1

RESULT 9
 LOCUS A0011413 40 bp mRNA linear EST 03-AUG-1998
 DEFINITION A0011413 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe cDNA clone spc11252, mRNA sequence.
 ACCESSION A0011413
 VERSION A0011413.1 GI:3356322
 KEYWORDS
 SOURCE EST.
 ORGANISM
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 1 (bases 1 to 40)
 Morlmyo, M. and Mita, K.
 Identification of expressed sequence tags of Schizosaccharomyces
 pombe
 Unpublished (1998)
 Contact: Mitsunori Morlmyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morlmyo@nirs.go.jp
 Location/Qualifiers
 1..40
 /organism="Schizosaccharomyces pombe"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc11252"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 12 a 10 c 9 g 9 t

ORIGIN

Query Match 55.4%; Score 14.4; DB 9; Length 40;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 ACTCAGCAGCTGATTAAGCAGA 25
 ||||| ||||| ||||| |||||
 DB 6 ACTCAGCGCTGAACCTTAAGCATA 29

RESULT 10
 LOCUS A2918464 84 bp DNA linear GSS 17-DEC-2001
 DEFINITION 1006004D07.x3 1006 - Rescemu Grid G Zea mays genomic DNA
 sequence.
 ACCESSION A2918464
 VERSION A2918464.1 GI:13387748
 KEYWORDS
 SOURCE GSS.
 ORGANISM
 Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1 (bases 1 to 84)
 Maize genomic sequences found using engineered Rescemu transposon
 Walbot, V.
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by a single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1006004 row: 36
 Class: transposon tagged.
 Location/Qualifiers
 1..84
 /organism="Zea mays"
 /cultivar="mixed background W23/Al88/B73"
 /db_xref="taxon:4577"
 /clone_lib="1006 - Rescemu Grid G"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf; Vector: Rescemu (engineered from
 pBluescript backbone); Site_1: BamHI; Site_2: BglII;
 Rescemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescemu, go to the web
 site 'www.zmdb.lastate.edu' and follow the links for
 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

BASE COUNT 29 a 13 c 31 g 11 t

ORIGIN

Query Match 55.4%; Score 14.4; DB 17; Length 84;
 Best Local Similarity 75.0%; Pred. No. 1.6e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 CTCAGCAGCTGATTAAGCAGAG 26
 ||||| ||||| ||||| |||||
 DB 61 CTCAGCAGCTTGCTTTAAACAGCG 84

RESULT 11
 LOCUS AA721220 91 bp mRNA linear EST 23-JAN-1998
 DEFINITION AA721220.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1300631 3',
 mRNA sequence.
 ACCESSION AA721220
 VERSION AA721220.1 GI:2737355
 KEYWORDS
 SOURCE EST.
 ORGANISM
 Human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Altman,
 Ph.D., Gerald Marfi, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bernaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrip/image/image.html
 Insert Length: 1195 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from AmerSham
 High quality sequence stop: 87.

FEATURES

source

```

1. .91
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_idb="NCI-CGAP-GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CHBR). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCGATTTTGTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

BASE COUNT

15 a 24 c 35 g 17 t

ORIGIN

Query Match 55.4%; Score 14.4; DB 9; Length 91;
 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 CTCAGCCACTGATTTAGCAG 26
 ||||| ||||| |||||
 Db 58 CTCAGCCAGGCGTCTTAACAGTG 81

RESULT 12
 AI536504 100 bp mRNA linear EST 18-MAR-1999
 LOCUS AI536504
 DEFINITION VP05606.V1 Soares_mammary_gland_NBMWG Mus musculus cDNA clone
 IMAGE:1067723 5', mRNA sequence.

ACCESSION AI536504
 VERSION AI536504.1 GI:4450639
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 100)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:590083

FEATURES
 source
 1. .100
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"

Query Match 54.6%; Score 14.2; DB 12; Length 75;
 Best Local Similarity 84.2%; Pred. No. 1.9e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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/clone="IMAGE:1067723"
/clone_idb="Soares_mammary_gland_NBMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker. Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGATTTTGTTTTGTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

```

BASE COUNT

19 a 23 c 40 g 18 t

ORIGIN

Query Match 55.4%; Score 14.4; DB 9; Length 100;
 Best Local Similarity 75.0%; Pred. No. 1.8e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGATTTAGCAG 24
 ||||| ||||| |||||
 Db 28 CACACAGCTGCTGATTCACGCTG 51

RESULT 13

LOCUS BG408667 75 bp mRNA linear EST 13-MAR-2001
 DEFINITION dd03f10.y1 NICHD XGC 001 xenopus laevis cDNA clone IMAGE:3405475
 5', mRNA sequence.

ACCESSION BG408667
 VERSION BG408667.1 GI:13315016
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis

REFERENCE 1 (bases 1 to 75)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Seq primer: -40RP from Gibco.

FEATURES

source

```

1. .75
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3405475"
/clone_idb="NICHD XGC 001"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."

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BASE COUNT

38 a 10 c 18 g 9 t

ORIGIN

Query Match 54.6%; Score 14.2; DB 12; Length 75;
 Best Local Similarity 84.2%; Pred. No. 1.9e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 773.192 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-1
Perfect score: 54
Sequence: 1 TAAATTAATACGACTGCTCA.....CCCTGAGGCTCAAGTCAGA 54

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl :
1: gb_da : *
2: gb_hlg : *
3: gb_in : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vl : *
15: em_da : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_om : *
21: em_or : *
22: em_ov : *
23: em_pat : *
24: em_ph : *
25: em_pl : *
26: em_ro : *
27: em_sts : *
28: em_un : *
29: em_vl : *
30: em_hlg_hum : *
31: em_hlg_liv : *
32: em_hlg_other : *
33: em_hlg_mus : *
34: em_hlg_pin : *
35: em_hlg_rod : *
36: em_hlg_mam : *
37: em_hlg_vtl : *
38: em_sy : *
39: em_hlgo_hum : *
40: em_hlgo_mus : *
41: em_hlgo_other : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	31.8	58.9	51	6	AX397806 Sequence
2	31	57.4	49	6	AR061368 Sequence
3	31	57.4	49	6	AR108267 Sequence
4	31	57.4	49	6	II6224 Sequence
5	31	57.4	49	6	II6224 Sequence
6	31	57.4	49	6	II6710 Sequence
7	31	57.4	49	6	II6710 Sequence
8	31	57.4	49	6	AR061668 Sequence
9	31	57.4	49	6	AR108567 Sequence
10	31	57.4	49	6	II65104 Sequence
11	30.8	57.0	49	6	II6633 Sequence
12	30.8	57.0	49	6	II6634 Sequence
13	30.8	57.0	49	6	II6635 Sequence
14	30.2	55.9	52	6	AX166846 Sequence
15	30	55.6	55	6	AX397811 Sequence
16	29.8	55.2	51	6	AR153317 Sequence
17	29.6	54.8	60	6	II5073 Sequence
18	29.4	54.4	36	6	AX045344 Sequence
19	29.4	54.4	49	6	AR207661 Sequence
20	29.4	54.4	50	6	E61335 Sequence
21	29.4	54.4	56	6	AX019749 Sequence
22	29.4	54.4	62	6	AX080569 Sequence
23	29.4	54.4	65	6	AX019769 Sequence
24	29.4	54.4	67	6	AX089393 Sequence
25	29.4	54.4	70	6	AX019760 Sequence
26	29.4	54.4	91	6	AX019756 Sequence
27	29.4	54.4	96	6	AX009277 Sequence
28	29.4	54.4	99	6	II5071 Sequence
29	29	53.7	37	6	E61325 Sequence
30	29	53.7	45	6	E61325 Sequence
31	29	53.7	47	6	AR070666 Sequence
32	29	53.7	47	6	AR157485 Sequence
33	29	53.7	47	6	II5930 Sequence
34	29	53.7	50	6	AR102985 Sequence
35	29	53.7	59	6	II5069 Sequence
36	28.8	53.3	48	6	AX147895 Sequence
37	28.6	53.0	48	6	AX147924 Sequence
38	28.6	53.0	71	6	AX451979 Sequence
39	28.6	53.0	71	6	AX458692 Sequence
40	28.6	53.0	77	6	AX451980 Sequence
41	28.4	52.6	56	6	AX458693 Sequence
42	28.4	52.6	56	6	AX278217 Sequence
43	28.4	52.6	88	6	BD012958 Sequence
44	28.4	52.6	88	6	E37843 Sequence
45	28.4	52.6	88	23	BD008384 Sequence

ALIGNMENTS

RESULT 1
AX397806
LOCUS AX397806
DEFINITION Sequence 40 from Patent WO0220852.
ACCESSION AX397806
VERSION AX397806.1 GI:21260680
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 40 14-MAR-2002

REFERENCE 1 (bases 1 to 49)
AUTHORS Gold, L. and Tuerk, C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 5696249-A 50 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..49
BASE COUNT 18 a 10 c 8 g 13 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCCTATAGGAGACTCAGACCCCTGAGGCTCAAGTCA 52
DB 1 TAATAGACTCCTATAGGAGACTCAGACCTTTTAATCTGACATCA 47

RESULT 7
AR061668
LOCUS Sequence 350 from patent US 5843653.
DEFINITION AR061668
ACCESSION AR061668
VERSION AR061668.1 GI:5989359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gold, L. and Tuerk, C.
TITLE Method for detecting a target molecule in a sample using a nucleic acid ligand
JOURNAL Patent: US 5843653-A 350 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..73
BASE COUNT 27 a 13 c 10 g 23 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCCTATAGGAGACTCAGACCCCTGAGGCTCAAGTCA 52
DB 1 TAATAGACTCCTATAGGAGACTCAGACCTTTTAATCTGACATCA 47

RESULT 8
AR108567
LOCUS Sequence 350 from patent US 6110900.
DEFINITION AR108567
ACCESSION AR108567
VERSION AR108567.1 GI:12824054
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gold, L. and Tuerk, C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 6110900-A 350 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..73
BASE COUNT 27 a 13 c 10 g 23 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCCTATAGGAGACTCAGACCCCTGAGGCTCAAGTCA 52
DB 1 TAATAGACTCCTATAGGAGACTCAGACCTTTTAATCTGACATCA 47

RESULT 9
I85104
LOCUS Sequence 350 from patent US 5696249.
DEFINITION I85104
ACCESSION I85104
VERSION I85104.1 GI:3022624
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gold, L. and Tuerk, C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 5696249-A 350 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..73
BASE COUNT 27 a 13 c 10 g 23 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCCTATAGGAGACTCAGACCCCTGAGGCTCAAGTCA 52
DB 1 TAATAGACTCCTATAGGAGACTCAGACCTTTTAATCTGACATCA 47

RESULT 10
I40633
LOCUS Sequence 5 from patent US 5622827.
DEFINITION I40633
ACCESSION I40633
VERSION I40633.1 GI:2082113
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 49)
AUTHORS McAllister, D.L. and Clark, K.A.
TITLE Amplification primers and nucleic acid probes targeted to coccidioides immitis nucleic acid
JOURNAL Patent: US 5622827-A 5 22-APR-1997;
FEATURES Location/Qualifiers
source 1..49
BASE COUNT 16 a 13 c 9 g 11 t
ORIGIN

Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35; 2; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 2;

QY 2 AAATTAATAGACTCCTATAGGAGACTCAGAC 35
DB 1 AAATTAATAGACTCCTATAGGAGACTCAGAC 34

RESULT 11
I40634
LOCUS Sequence 6 from patent US 5622827.
DEFINITION I40634
ACCESSION I40634
VERSION I40634.1 GI:2082114
KEYWORDS
SOURCE Unknown.

```

ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 49)
TITLE McAllister,D.L. and Clark,K.A.
JOURNAL Amplification primers and nucleic acid probes targeted to
FEATURES coccidioides immitis nucleic acid
          Patent: US 5622827-A 6 22-APR-1997;
          Location/Qualifiers
            source
              1..49
              /organism="unknown"
BASE COUNT 11 a 9 c 13 g 16 t
ORIGIN
Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAATTAATACGACTCCTATAGGAGACACAGAC 35
Db 49 AAATTAATACGACTCCTATAGGAGACACAGAC 16

RESULT 12
LOCUS 140635 49 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 7 from patent US 5622827.
ACCESSION 140635
VERSION 140635.1 GI:2082115
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS McAllister,D.L. and Clark,K.A.
TITLE Amplification primers and nucleic acid probes targeted to
JOURNAL coccidioides immitis nucleic acid
FEATURES Patent: US 5622827-A 7 22-APR-1997;
          Location/Qualifiers
            source
              1..49
              /organism="unknown"
BASE COUNT 16 a 13 c 9 g 11 t
ORIGIN
Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAATTAATACGACTCCTATAGGAGACACAGAC 35
Db 1 AAATTAATACGACTCCTATAGGAGACACAGAC 34

RESULT 13
LOCUS 140636 49 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 8 from patent US 5622827.
ACCESSION 140636
VERSION 140636.1 GI:2082116
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS McAllister,D.L. and Clark,K.A.
TITLE Amplification primers and nucleic acid probes targeted to
JOURNAL coccidioides immitis nucleic acid
FEATURES Patent: US 5622827-A 8 22-APR-1997;
          Location/Qualifiers
            source
              1..49
              /organism="unknown"
BASE COUNT 11 a 9 c 13 g 16 t
ORIGIN

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Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAATTAATACGACTCCTATAGGAGACACAGAC 35
Db 49 AAATTAATACGACTCCTATAGGAGACACAGAC 16

RESULT 14
LOCUS AX166846 52 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 12 from Patent WO0144510.
ACCESSION AX166846
VERSION AX166846.1 GI:14596449
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 52)
AUTHORS Brenzano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
          Rodrique,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 12 21-JUN-2001;
          Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES Location/Qualifiers
          source
            1..52
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="primer oligonucleotide"
BASE COUNT 17 a 14 c 11 g 10 t
ORIGIN
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Best Local Similarity 81.4%; Pred. No. 0.59;
Matches 33; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2 AAATTAATACGACTCCTATAGGAGACACAGCCCTAGGCT 44
Db 2 AAATTAATACGACTCCTATAGGAGACACAGCATCAGGCT 44

RESULT 15
LOCUS AX397811 55 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 45 from Patent WO0220852.
ACCESSION AX397811
VERSION AX397811.1 GI:21260685
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Yang,Y.Y., Brenzano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of hiv-1 sequences for detection of sequences
          associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 45 14-MAR-2002;
          Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES Location/Qualifiers
          source
            1..55
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Oligonucleotide primer for Reverse Transcriptase
            target sequence"
BASE COUNT 17 a 16 c 9 g 13 t
ORIGIN
Query Match 55.6%; Score 30; DB 6; Length 55;
Best Local Similarity 86.8%; Pred. No. 0.71;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

• Mon, Dec 23 08:47:52 2002

us-09-121-239-1.rge

Page 5

QY 2 AAATTATACGACTCTATATAGGAGACTCAGACCTG 39
|||||
Db 2 AAATTATACGACTCTATATAGGAGACTCAGACCTG 39
|||||

Search completed: December 21, 2002, 12:57:14
Job time : 781.192 secs

11

11

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 343.641 Seconds
(without alignments)
2032.551 Million cell updates/sec

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Title: US-09-121-239-5
Perfect score: 24
Sequence: 1 GACCAACTCGTGTGTGAACCTCCA 24
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters:
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Minimum DB seq length: 0
Maximum DB seq length: 100
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database :

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GenEmbl1:*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pt.*
10: gb_rs.*
11: gb_st.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_cm.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_st.*
28: em_un.*
29: em_vl.*
30: em_hg_hum.*
31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hg_mus.*
34: em_hg_dln.*
35: em_hg_rnd.*
36: em_hg_man.*
37: em_hg_yrl.*
38: em_sy.*
39: em_hgo_hum.*
40: em_hgo_mus.*
41: em_hgo_other.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	24	6	E61323	E61323 Probe for d
2	24	87.5	40	6	AR100696	AR100696 Sequence
3	20	83.3	20	6	183631	183631 Sequence 5
4	16	66.7	40	6	E16986	E16986 Sense prime
5	14.6	60.8	100	11	HSPE85A07	A0008643 R.sapiens
6	14	58.3	33	6	AR027112	AR027112 Sequence
7	14	58.3	67	6	AR039996	AR039996 Sequence
8	13.8	57.5	90	11	AGRP6323	Z68675 A.gambiae S
9	13.6	56.7	46	6	AR168044	AR168044 Sequence
10	13.6	56.7	46	6	AR204815	AR204815 Sequence
11	13.6	56.7	48	6	AX221595	AX221595 Sequence
12	13.6	56.7	48	6	AX274567	AX274567 Sequence
13	13.6	56.7	48	6	AX426270	AX426270 Sequence
14	13.6	56.7	76	12	AY044144	AY044144 Synthetic
15	13.6	56.7	93	10	MMTCRDJ7	X64902 M.musculus
16	13.4	55.8	32	6	AR050567	AR050567 Sequence
17	13.4	55.8	82	9	HSMTGAB1	Z22683 H.sapiens T
18	13.4	55.8	93	5	SMSCAT2	X93900 S.melanotie
19	13.4	55.8	95	6	AR166860	AR166860 Sequence
20	13.4	55.8	95	6	AX192486	AX192486 Sequence
21	13.2	55.0	30	6	AX255417	AX255417 Sequence
22	13.2	55.0	31	6	AX255416	AX255416 Sequence
23	13.2	55.0	32	6	AX356286	AX356286 Sequence
24	13	54.2	20	6	AX353365	AX353365 Sequence
25	13	54.2	20	6	E23800	E23800 Method for
26	13	54.2	27	6	AR188058	AR188058 Sequence
27	13	54.2	27	6	AR189481	AR189481 Sequence
28	13	54.2	56	6	AR038824	AR038824 Sequence
29	13	54.2	56	6	E146850	E146850 Sequence 11
30	13	54.2	78	6	A59428	A59428 Sequence 21
31	13	54.2	78	6	AR182182	AR182182 Sequence
32	13	54.2	90	6	HUMGRAS09	D26524 Homo sapien
33	13	54.2	98	6	AR017637	AR017637 Sequence
34	13	54.2	98	6	AR094814	AR094814 Sequence
35	13	54.2	98	6	AR155473	AR155473 Sequence
36	13	54.2	98	6	AX094953	AX094953 Sequence
37	12.8	53.3	21	6	A58045	A58045 Sequence 54
38	12.8	53.3	24	6	AR176486	AR176486 Sequence
39	12.8	53.3	32	6	AX214324	AX214324 Sequence
40	12.8	53.3	37	6	AR176480	AR176480 Sequence
41	12.8	53.3	37	6	A59456	A59456 Sequence 3
42	12.8	53.3	47	6	AX194760	AX194760 Sequence
43	12.8	53.3	51	6	AX158736	AX158736 Sequence
44	12.8	53.3	79	8	OE031700	AT311700 Oles euro
45	12.8	53.3	86	6	AR045036	AR045036 Sequence

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
E61323	E61323	Probe for detecting oligonucleotide.	E61323	E61323.1 GI:13025885	JP 1999046778-A/37.	synthetic construct.	artificial sequences.	1 (bases 1 to 24)	Daniel, L.K. and Timothy J.F.	Probe for detecting oligonucleotide
									Patent: JP 1999046778-A 37 23-FEB-1999;	
									GEN-PROBE INC	

COMMENT OS Artificial Sequence
PN JP 199046778-A/37
PD 23-FEB-1999
PF 14-JAN-1998 JP 1998005607
PR 11-JUL-1989 US 379501
PI DANIEL LOUIS KASHIAN, TIMOTHY J FURUTSU
PC C12N15/09, C12Q1/68, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1.24
FT Location/Qualifiers

FEATURES
source 1.24
Location/Qualifiers
1.24
/Organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 7 a 7 c 5 g 5 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACCACTCGTGTGAACTCA 24
DB 1 GACCACTCGTGTGAACTCA 24

RESULT 2
ARI00696 40 bp DNA linear PAT 14-FEB-2001
LOCUS ARI00696
DEFINITION Sequence 16 from patent US 6080851.
ACCESSION ARI00696
VERSION ARI00696.1 GI:12811144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Pachuk, C.J., Coney, L.R. and Oakes, F.T.
TITLE Ribozymes with linked anchor sequences
JOURNAL Patent: US 6080851-A 16 27-JUN-2000;
FEATURES
source 1.40
Location/Qualifiers
1.40
/organism="unknown"

BASE COUNT 12 a 7 c 9 g 12 t
ORIGIN

Query Match 87.5%; Score 21; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CAACCTCGTGTGAACTCA 24
DB 20 CAACCTCGTGTGAACTCA 40

RESULT 3
183631 20 bp DNA linear PAT 10-AUG-1998
LOCUS 183631
DEFINITION Sequence 5 from patent US 5714383.
ACCESSION 183631
VERSION 183631.1 GI:3407161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Thompson, J.D.
TITLE Method and reagent for treating chronic myelogenous leukemia
JOURNAL Patent: US 5714383-A 5 03-FEB-1998;
FEATURES
source 1.20
Location/Qualifiers
1.20
/organism="unknown"

BASE COUNT 5 a 6 c 4 g 5 t
ORIGIN

Query Match 83.3%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CAACCTCGTGTGAACTCC 23
DB 1 CAACCTCGTGTGAACTCC 20

RESULT 4
E16986 40 bp DNA linear PAT 28-JUL-1999
LOCUS E16986
DEFINITION Sense primer for detection of major-bcr.
ACCESSION E16986
VERSION E16986.1 GI:5711669
KEYWORDS JP 1998229899-A/1.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 40)
AUTHORS Kobayashi, M., Kawaguchi, R., Segawa, M. and Takarada, Y.
TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA, AND DETECTION OF BCR/ABL TYPE CHIMERA MESSENGER RNA USING THE SAME
JOURNAL Patent: JP 1998229899-A 1 08-SEP-1998;
S R L:KK, TOYOBO CO LTD
OS None
OC Artificial sequences.
PN JP 1998229899-A/1
PD 02-SEP-1998
PE 21-FEB-1997 JP 1997054092
PI KOBAYASHI MASARU, KAWAGUCHI RYUJI, SEGAWA MASAYA, PI TAKARADA YUTAKA
PC C12Q1/68, G01N33/50//C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH 1.40
FT source 1.40
FT Location/Qualifiers
1.40
/organism="Artificial sequences".

FEATURES
source 1.40
Location/Qualifiers
1.40
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 9 a 13 c 9 g 9 t
ORIGIN

Query Match 66.7%; Score 16; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 CGTGTGTGAACTCA 24
DB 1 CGTGTGTGAACTCA 16

RESULT 5
HSP35A07 100 bp DNA linear STS 21-MAY-1998
LOCUS HSP35A07
DEFINITION H. sapiens flow-sorted chromosome 1 HindIII fragment, SCIP35A07, sequence tagged site.
ACCESSION AL009849
VERSION AL009849.1 GI:2665012
KEYWORDS STS: single read.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Gregory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E.
TITLE Direct Submission

JOURNAL Submitted (03-DEC-1997) E-mail contact: hunqueresanger.ac.uk
COMMENT Vector: pBSITK+
Marker: STG32823FS (Primer A: CTTAAACACCAACCTCTGCG; Primer B: AGCTGCTTTCAGAAATCA; amplicon size: 86 bp) was mapped to chromosome 1 using Radiation Hybrid panel Genebridge 4 (GB4).

FEATURES
source
1. 100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="SC1P35A07"
/sex="Female"
/tissue_type="EBV lymphoblastoid cell line"
/clone_id="SC1P"
/dev_stage="adult"

BASE COUNT 29 a 27 c 24 g 20 t

ORIGIN
Query Match 60.8%; Score 14.6; DB 11; Length 100;
Best Local Similarity 81.0%; Pred. No. 2.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 CAACTGCTGTGTGAACCTCA 24
||| ||| ||| ||| ||| |||
Db 24 CAGCTGCTGTGTGAAGGCCA 44

RESULT 6
LOCUS AR027112 33 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5856153.
ACCESSION AR027112
VERSION AR027112.1 GI:5937952
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Tiraby,G., Reyes,J.-P., Tiraby,M., Cazaux,C. and Drocourt,D.
TITLE Suicide genes and new associations of pyrimidine nucleobase and nucleoside analogs with new suicide genes for gene therapy of acquired diseases
JOURNAL Patent: US 5856153-A 12 05-JAN-1999;
FEATURES
source
1. 33
/organism="unknown"
BASE COUNT 6 a 15 c 4 g 8 t

ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 33;
Best Local Similarity 77.3%; Pred. No. 5.8e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 ACCAACTGCTGTGTGAACCTC 23
||||| ||| ||| ||| ||| |||
Db 9 ACCATCTCATGCTCCCACTCC 30

RESULT 7
LOCUS AR139996 60 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 3 from patent US 6207419.
ACCESSION AR139996
VERSION AR139996.1 GI:14482492
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 60)
AUTHORS Church,F.C. and Bauman,S.J.
TITLE Thrombin inhibitory agents and methods of using same
JOURNAL Patent: US 6207419-A 3 27-MAR-2001;

FEATURES
source
Location/Qualifiers
1. 60
/organism="unknown"
BASE COUNT 16 a 6 c 22 g 16 t

ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 60;
Best Local Similarity 77.3%; Pred. No. 5.3e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CCAACTGCTGTGTGAACCTCA 24
||||| ||| ||| ||| ||| |||
Db 59 CCAACCTGTGTGTAAAGCACA 38

RESULT 8
LOCUS AGRP03273 97 bp DNA linear STS 16-JAN-1996
DEFINITION A.gambiae STS DNA (RAPD32; 73 end, sequence tagged site).
ACCESSION 268675
VERSION 268675.1 GI:1159930
KEYWORDS STS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
REFERENCE 1 (bases 1 to 97)
AUTHORS Dimopoulos,G., Zheng,L., Kumar,V., della Torre,A., Kafatos,F.C. and Louis,C.
JOURNAL Unpublished
DEFINITION 2 (bases 1 to 97)
ACCESSION Dimopoulos,G.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-1996) Georg Dimopoulos, IMB, Foundation for Research and Technology, Hellas, Solonos 2, P.O.Box 1527, 711 10 Heraklion, Greece
REFERENCE 3 (bases 1 to 97)
AUTHORS Dimopoulos,G., Zheng,L., Kumar,V., della Torre,A., Kafatos,F.C. and Louis,C.
TITLE Integrated genetic map of Anopheles gambiae: use of RAPD polymorphisms for genetic, cytogenetic and STS landmarks
JOURNAL Genetics 143 (2), 953-960 (1996)
MEDLINE 96363927
PUBMED 8725241
FEATURES
source
Location/Qualifiers
1. 97
/organism="Anopheles gambiae"
/strain="GASUA"
/db_xref="taxon:7165"
/chromosome="2"
/map="18D"
/clone="RAPD32"
/dev_stage="adult"
1. 97
/note="sequenced from T3 promotor; distinguishes strain GASUA from WE; Length of RAPD32: ca. 500 bp"

STSS
primer_bind
1. 10
/note="PCR primer"
BASE COUNT 35 a 19 c 15 g 28 t

ORIGIN
Query Match 57.5%; Score 13.8; DB 11; Length 97;
Best Local Similarity 88.2%; Pred. No. 6.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACCAACTGCTGTGTGAA 18
||||| ||| ||| ||| ||| |||
Db 75 ACCAATGCTGTGTGAA 91

RESULT 9
LOCUS AR168044/c

LOCUS AR168044 46 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 19 from patent US 6287788.
ACCESSION AR168044
VERSION AR168044.1 GI:17903862
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Bard,J.A., Borowsky,B., Smith,K.E., Branchek,T.A., Gerald,C.P.G.
and Jones,K.A.
TITLE DNA encoding galanin GALR3 receptors and uses thereof
JOURNML Patent: US 6287788-A 19 11-SEP-2001;
FEATURES location/Qualifiers
source 1..46 /organism="unknown"
BASE COUNT 15 a 7 c 17 g 7 t
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 46;
Best Local Similarity 80.0%; Pred. No. 8.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CCAACTCGTGTGGAACCTC 22
||||| ||||| |||||
Db 39 CCAACTCCTGTGTCAACCCC 20
RESULT 10
LOCUS AR204815 46 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from patent US 6368812.
ACCESSION AR204815
VERSION AR204815.1 GI:21502237
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Bard,J.A., Borowsky,B., Smith,K.E., Branchek,T.A., Gerald,C.P.G.
and Jones,K.A.
TITLE Process for determining the agonist or antagonist of galanin
receptor (GALR3)
JOURNML Patent: US 6368812-A 19 09-APR-2002;
FEATURES location/Qualifiers
source 1..46 /organism="unknown"
BASE COUNT 15 a 7 c 17 g 7 t
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 46;
Best Local Similarity 80.0%; Pred. No. 8.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CCAACTCGTGTGGAACCTC 22
||||| ||||| |||||
Db 39 CCAACTCCTGTGTCAACCCC 20
RESULT 11
LOCUS AX221595 48 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 7037 from Patent WO0159103.
ACCESSION AX221595
VERSION AX221595.1 GI:15549319
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 48)
AUTHORS Blatt,L., Mcswigen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression

JOURNAL Patent: WO 0159103-A 7037 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
Mcswigen, James (US) ; Chowrira, Bharat M. (US)
FEATURES location/Qualifiers
source 1..48 /organism="synthetic construct"
BASE COUNT 14 a 13 c 12 g 9 t
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 8.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 CCAACTCGTGTGGAACCTC 23
||||| ||||| |||||
Db 1 CAGCTCGTGAGGAACCTCC 20
RESULT 12
LOCUS AX274567 48 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 2136 from Patent WO0162911.
ACCESSION AX274567
VERSION AX274567.1 GI:16547306
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 48)
AUTHORS Jarvis,T., von Carlowitz,I., Mcswigen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNML Patent: WO 0162911-A 2136 30-AUG-2001;
FEATURES location/Qualifiers
source 1..48 /organism="synthetic construct"
BASE COUNT 11 a 16 c 12 g 9 t
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 8.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 CCAACTCGTGTGGAACCTC 23
||||| ||||| |||||
Db 1 CAGCTCGTGAGGAACCTCC 20
RESULT 13
LOCUS AX426270 48 bp mRNA linear PAT 18-JUN-2002
DEFINITION Sequence 4606 from Patent WO0186124.
ACCESSION AX426270
VERSION AX426270.1 GI:21529656
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 48)
AUTHORS Jarvis,T., von Carlowitz,I., Mcswigen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNML Patent: WO 0186124-A 4606 22-NOV-2001;
FEATURES location/Qualifiers
source 1..48 /organism="synthetic construct"
/db_xref="taxon:32630"

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BASE COUNT      10 a      15 c      15 g      8 t
ORIGIN
Query Match      56.7%; Score 13.6; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 8.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4  CACCTCGTGTGGAACCTCC 23
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Db       1  CACCTCGTGTGGAACCTCC 20

RESULT 14
LOCUS      AY044144
DEFINITION Synthetic construct motif I cis element sequence.
ACCESSION  AY044144
VERSION    AY044144.1 GI:15625235
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 76)
AUTHORS   Peng, R., Yao, Q., Xiong, A., Li, X. and Fan, H.
TITLE     Direct Submission
JOURNAL   Submitted (06-JUL-2001) Shanghai Yong Ye Agro-Bioengineering Co.,
          Ltd, Shanghai Academy of Agricultural Sciences, Beid Road 2901,
          Shanghai 201106, China
FEATURES   location/Qualifiers
            1..76
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="contains three copies of the motif I element
            (AGTACGTGCGC); can be inserted into lacZ reporter plasmid
            for yeast one-hybrid system"
BASE COUNT      19 a      20 c      23 g      14 t
ORIGIN
Query Match      56.7%; Score 13.6; DB 12; Length 76;
Best Local Similarity 80.0%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2  ACCAACTCGTGTGGAAC 21
         ||| ||||| |||||
Db       37  ACCAACTCGTGTGGAAC 18

RESULT 15
LOCUS      MMTCRVDDJ
DEFINITION M.musculus rearranged TCR delta gene V-p-lambda-12, D-delta-1,
ACCESSION  X64902
VERSION    X64902.1 GI:54746
KEYWORDS   antigen receptor; D-region; delta gene; J-region; T cell receptor;
SOURCE     V-region.
ORGANISM   Mus musculus.
REFERENCE  1 (bases 1 to 93)
AUTHORS   Chien, Y.H., Iwashima, M., Wettstein, D.A., Kaplan, K.B., Elliott, J.F.,
          Born, W. and Davis, M.M.
TITLE     T-cell receptor delta gene rearrangements in early thymocytes
JOURNAL   Nature 330, 24-31 (1987)
COMMENT   See also X63933-9 & X64900-3.
FEATURES   location/Qualifiers
            1..93
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /cell_type="thymocytes"
            /dev_stage="18-19 day fetus"

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misc_feature      1..24
                  /note="V region"
misc_feature      25..31
                  /note="D delta 1 region"
misc_feature      34..40
                  /note="D delta 2 region"
misc_feature      45..93
                  /note="J delta 1 region"
BASE COUNT      25 a      25 c      22 g      21 t
ORIGIN
Query Match      56.7%; Score 13.6; DB 10; Length 93;
Best Local Similarity 80.0%; Pred. No. 7.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GACCAACTCGTGTGGAAC 20
         ||| ||||| |||||
Db       48  GACCAACTCGTGTGGAAC 67

Search completed: December 21, 2002, 12:57:24
Job time : 353.641 secs

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source 1..56
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BASE COUNT 18 a 18 c 9 g 11 t

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
|||||

Db 3 GACTGTCCACAGCATTCGCGTGACC 27

RESULT 2
LOCUS 114509
DEFINITION Sequence 17 from patent US 5451503.
ACCESSION 114509
VERSION 114509.1 GI:996992
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J., Jr., Nelson,N.C. and Bezverkov,R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 17 19-SEP-1995;
FEATURES Location/Qualifiers
source 1..56
/organism="unknown"

BASE COUNT 18 a 18 c 9 g 11 t

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
|||||

Db 3 GACTGTCCACAGCATTCGCGTGACC 27

RESULT 3
LOCUS 183632
DEFINITION Sequence 6 from patent US 5714383.
ACCESSION 183632
VERSION 183632.1 GI:3407162
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 26)
AUTHORS Thompson,J.D.
TITLE Method and reagent for treating chronic myelogenous leukemia
JOURNAL Patent: US 5714383-A 6 03-FEB-1998;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"

BASE COUNT 6 a 10 c 5 g 5 t

ORIGIN

Query Match 96.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGAC 24
|||||

Db 3 GACTGTCCACAGCATTCGCGTGAC 26

RESULT 4

E16986
LOCUS 40 bp DNA linear PAT 28-JUL-1999
DEFINITION Sense primer for detection of major-bcr.
ACCESSION E16986
VERSION E16986.1 GI:5711669
KEYWORDS JP 1998229899-A/1.
SOURCE unidentified.
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 40)
AUTHORS Kobayashi,M., Kawaguchi,R., Segawa,M. and Takarada,Y.
TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA, AND
JOURNAL DETECTION OF BCR/ABL TYPE CHIMERA MESSENGER RNA AND USING THE SAME
PATENT: JP 1998229899-A 1 02-SEP-1998;
COMMENT S R L:KK, TOYOBO CO LTD
OS None
OC Artificial sequences.
PN JP 1998229899-A/1
PD 02-SEP-1998
PF 21-FEB-1997 JP 1997054092
PI KOBAYASHI MASARU, KAWAGUCHI RYUJI, SEGAWA MASAYA, PI
TAKARADA YUTAKA
PC C1201/68, G01N33/50//C12N15/09;
CC strandedness: Single;
FH topology: Linear;
FT source Location/Qualifiers
FT 1..40 /organism="Artificial sequences".

FEATURES
source Location/Qualifiers
1..40 /organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 9 a 13 c 9 g 9 t

ORIGIN

Query Match 96.0%; Score 24; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGAC 24
|||||

Db 17 GACTGTCCACAGCATTCGCGTGAC 40

RESULT 5
LOCUS AX003487/c 39 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 67 from Patent WO9928439.
ACCESSION AX003487
VERSION AX003487.1 GI:9927340
KEYWORDS
SOURCE B19 virus.
ORGANISM B19 virus.
REFERENCE 1 (bases 1 to 39)
AUTHORS Auguste,V., Garbarg-Chenon,A. and Nguyen,Q.T.
TITLE Erythrovirus and its applications
JOURNAL Patent: WO 9928439-A 67 10-JUN-1999;
ASSIST PUBL HOPITAUX DE PARIS (FR); AUGUSTE VERONIQUE (FR); GARBARG
CHENON ANTOINE (FR); NGUYEN QUANG TRI (FR)
FEATURES Location/Qualifiers
source 1..39
/organism="B19 virus"
/db_xref="taxon:10798"

BASE COUNT 8 a 11 c 13 g 7 t

ORIGIN

Query Match 75.2%; Score 18.8; DB 6; Length 39;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGTCCACAGCATTCGCGTGA 23

Db 33 ACTGTCACAGCATTCGCTGACGA 12

RESULT 6
LOCUS 158643 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5652222.
ACCESSION 158643 GI:2477881
VERSION 158643.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 22)
TITLE Calabretta, B. and Gewirtz, A.M.
JOURNAL selective inhibition of leukemic cell proliferation by bcr-abl
FEATURES Patent: US 5652222-A 11 29-JUL-1997;
LOCATION/Qualifiers
source 1..22
BASE COUNT 6 a 9 c 3 g 4 t
ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACG 25
Db 1 CACAGCATTCGCTGACG 18

RESULT 7
LOCUS ARI00681 62 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6080851.
ACCESSION ARI00681
VERSION ARI00681.1 GI:12811129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 62)
TITLE Pachuk, C.J., Coney, L.R. and Oakes, F.T.
JOURNAL Ribozymes with linked anchor sequences
FEATURES Patent: US 6080851-A 1 27-JUN-2000;
LOCATION/Qualifiers
source 1..62
BASE COUNT 18 a 19 c 13 g 12 t
ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACG 25
Db 1 CACAGCATTCGCTGACG 18

RESULT 8
LOCUS ARI00682 81 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6080851.
ACCESSION ARI00682
VERSION ARI00682.1 GI:12811130
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 81)
TITLE Pachuk, C.J., Coney, L.R. and Oakes, F.T.
JOURNAL Ribozymes with linked anchor sequences
FEATURES Patent: US 6080851-A 2 27-JUN-2000;
LOCATION/Qualifiers
source 1..81
BASE COUNT 23 a 17 c 23 g 18 t
ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACG 25
Db 81 CACAGCATTCGCTGACG 64

RESULT 9
LOCUS A50293 60 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 13 from Patent WO9612803.
ACCESSION A50293
VERSION A50293.1 GI:2303347
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE
AUTHORS 1 (bases 1 to 60)
TITLE Blumenfeld, M.
JOURNAL METHOD FOR THE EX VIVO TREATMENT OF TUMOUR CELLS FROM PATIENTS WITH
COMMENT GENSET (FR)
FEATURES Other publication FR 2726004 960426.
LOCATION/Qualifiers
source 1..60
BASE COUNT 18 a 18 c 13 g 11 t
ORIGIN

Query Match 68.0%; Score 17; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACAGCATTCGCTGACG 25
Db 1 ACAGCATTCGCTGACG 17

RESULT 10
LOCUS ARI60054 28 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6251690.
ACCESSION ARI60054
VERSION ARI60054.1 GI:16222959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 28)
TITLE Kujala, S., Ala-Kleime, T., Eskola, J. and Korpele, T.
JOURNAL Electrical excitation of label substances at insulating film-coated
FEATURES Patent: US 6251690-A 2 26-JUN-2001;
LOCATION/Qualifiers
source 1..28
BASE COUNT 5 a 5 c 8 g 10 t
ORIGIN

Query Match 64.0%; Score 16; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 CAGCATTCGGCTGACC 25
 |||||
 DB 28 CAGCATTCGGCTGACC 13

RESULT 11
 E16784

LOCUS E16784 15 bp DNA linear PAT 28-JUL-1999
 DEFINITION PCR primer for detecting BCR EX3 mRNA.
 ACCESSION E16784
 VERSION E16784.1 GI:5711467
 KEYWORDS JP 1998215897-A/17.
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 15)
 Koshimoto, H., Sato, Y. and Tsuji, A.
 DETECTION OF MUTANT CELL BY CHROMOSOMAL RECIPROCAL TRANSLOCATION,
 PROBE KIT FOR THE SAME DETECTION AND DETECTOR THEREFOR
 Patent: JP 1998215897-A 17 18-AUG-1998;
 BUNSHI BIO PHOTONICS KENKYUSHO:KK

JOURNAL
 COMMENT OS None
 OC Artificial sequences.
 PN JP 1998215897-A/17
 PD 18-AUG-1998
 PF 05-FEB-1997 JP 1997022950

P1 KOSHIMOTO HIROYUKI, SATO YOSHIHIRO, TSUJI AKIHIKO PC
 C12Q1/68, C07H21/04, C12N15/09, G01N21/78;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH key Location/Qualifiers
 FT source 1..15
 FT Location/Qualifiers

FEATURES
 source 1..15
 Location/Qualifiers
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 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 3 a 6 c 3 g 3 t
 ORIGIN

Query Match 60.0%; Score 15; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CACAGCATTCGGCTG 22
 |||||
 DB 1 CACAGCATTCGGCTG 15

RESULT 12
 A28014/c

LOCUS A28014 54 bp DNA linear PAT 03-OCT-1995
 DEFINITION pCD4-FVCD3 construction oligo 2139.
 ACCESSION A28014
 VERSION A28014.1 GI:1248561
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM artificial construct.
 1 (bases 1 to 54)
 REFERENCE
 AUTHORS Karjalainen, K., Lantavacchia, A. and Trautnecker, A.
 TITLE Chimeric polypeptides
 JOURNAL Patent: EP 0505908-A 9 30-SEP-1992;
 F. HOFFMANN-LA ROCHE AG

FEATURES
 source 1..54
 Location/Qualifiers

BASE COUNT 11 a 9 c 22 g 12 t
 ORIGIN

Query Match 60.0%; Score 15; DB 6; Length 54;
 Best Local Similarity 78.3%; Pred. No. 1.3e+04;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CTGTCACAGCATTCGGCTGACC 25
 |||||

DB 32 CAGTCGACAGCATTCAGCTGACC 10

RESULT 13
 MCTR12

LOCUS MCTR12 77 bp mRNA linear BCT 31-MAR-1992
 DEFINITION Mycoplasma capricolum transfer RNA-ile (GAU).
 ACCESSION X16752
 VERSION X16752.1 GI:44246
 KEYWORDS transfer RNA; transfer RNA-ile.
 SOURCE Mycoplasma capricolum.
 ORGANISM Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 Entomoplasmataceae.

REFERENCE 1 (bases 1 to 77)
 Andachi, Y., Yamao, F., Muto, A. and Osawa, S.
 Codon recognition patterns as deduced from sequences of the
 complete set of transfer RNA species in Mycoplasma capricolum.
 Resemblance to mitochondria
 J. Mol. Biol. 209 (1), 37-54 (1989)

JOURNAL
 MEDLINE 90040718
 PUBMED 2478713

COMMENT See acc# X16741-X16769 for complete set of mycoplasma transfer
 RNA's.

FEATURES
 source 1..77
 Location/Qualifiers

1..77
 /organism="Mycoplasma capricolum"
 /strain="ATCC 27343 (Kid.)"
 /db_xref="taxon:2095"

1..77
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 /note="dihydrouridine"
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modified_base 20
 /note="dihydrouridine"
 /mod_base=d

modified_base 21
 /note="dihydrouridine"
 /mod_base=d

misc_feature 35..37
 /note="anylicodon (GAU)"
 38

modified_base 47
 /note="N-((9-beta-D-ribofuranosyl)purine-6-yl)
 carbamoyl)threonine"
 /mod_base=OTHER

modified_base 56
 /note="7-methylguanosine"
 /mod_base=m7g

modified_base 56
 /note="pseudouridine"
 /mod_base=p

BASE COUNT 20 a 17 c 20 g 20 t
 ORIGIN

Query Match 58.4%; Score 14.6; DB 1; Length 77;
 Best Local Similarity 81.0%; Pred. No. 2.1e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 CTGTCACAGCATTCGGCTGA 23
 |||

DB 16 CTGTTAGAGCATTCGGCTGA 36

```

RESULT 14
LOCUS       MMTNTI
DEFINITION  Mycoplasma mycoides sp. capri transfer RNA-ile (GAU).
ACCESSION   Y00372.1
VERSION     Y00372.1 GI:44470
KEYWORDS    transfer RNA; transfer RNA-ile.
SOURCE      Mycoplasma mycoides
ORGANISM    Mycoplasma mycoides
REFERENCE   1 (bases 1 to 77)
AUTHORS     Schoen, A.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-1987) Schoen, A., Yale University, Dept. MB+B, 260
            Whitney Ave., P.O. Box 6666, New Haven, CT 06511, USA
REFERENCE   2 (bases 1 to 77)
AUTHORS     Schoen, A.
TITLE       Sequence of an isoleucine tRNA from Mycoplasma mycoides sp. Capri
JOURNAL     Nucleic Acids Res. 15 (13), 5488 (1987)
MEDLINE     87260022
FEATURES
    source          1..77
                     /organism="Mycoplasma mycoides"
                     /strain="sp. capri"
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                     1..77
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                     /note="4-thiouridine"
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                     modified_base 20
                     /note="dihydrouridine"
                     /mod_base=d
                     modified_base 21
                     /note="dihydrouridine"
                     /mod_base=d
                     misc_feature 35..37
                     /note="anticodon (GAU)"
                     modified_base 38
                     /note="N-(9-beta-D-ribofuranosyl)purine-6-yl-(carbamoyl)threonine"
                     /mod_base=OTHER
                     modified_base 47
                     /note="7-methylguanosine"
                     /mod_base=m7g
                     modified_base 56
                     /note="pseudouridine"
                     /mod_base=p
BASE COUNT      20 a 17 c 20 g 20 t
ORIGIN
Query Match      58.4%; Score 14.6; DB 1; Length 77;
Best Local Similarity 81.0%; Pred. No. 2,1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 CTGTCACAGCATTCGCTGA 23
        ||| | |||||
Db      16 CTGCTAGACCATTCGCTGA 36

RESULT 15
LOCUS       AX460928/c
DEFINITION  Sequence 25 from Patent WO0238607.
ACCESSION   AX460928
VERSION     AX460928.1 GI:21726168
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.

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REFERENCE   1
AUTHORS     Aparicio, S., Carlton, M., Dixon, J., Messenger, S., Russ, A. and
            Thresher, R.
TITLE       A bacn 9 protein coupled receptor polypeptide and polynucleotide
            encoding this receptor
JOURNAL     Patent: WO 0238607-A 25 16-MAY-2002;
            Paradigm Therapeutics Limited (GB)
FEATURES
    source          1..35
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT      7 a 7 c 13 g 8 t
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Query Match      56.8%; Score 14.2; DB 6; Length 35;
Best Local Similarity 84.2%; Pred. No. 3,1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 ACTGTCACAGCATTCGCGC 20
        | |||| | |||||
Db      34 AGTGTCCCAAGCATTCGCGC 16

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Job time : 362.959 secs

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7
1

Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 : Search time 286.367 Seconds

(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-13

Perfect score: 20

Sequence: 1 CAAAGCAGCAGCAGCAGCAGC 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Capext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank

1: gb_da:*

2: gb_hg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_pl:*

8: gb_pl:*

9: gb_pl:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: gb_vl:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hg_hum:*

31: em_hg_inv:*

32: em_hg_other:*

33: em_hg_mus:*

34: em_hg_pln:*

35: em_hg_rtd:*

36: em_hg_mam:*

37: em_hg_vrt:*

38: em_sy:*

39: em_hgo_hum:*

40: em_hgo_mus:*

41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	78	6	AR052214 Sequence
2	17.4	87.0	96	6	AR052217 Sequence
3	17.4	87.0	96	6	AR194309 Sequence
4	14.8	74.0	66	6	AR052213 Sequence
5	14.8	74.0	69	6	AR052215 Sequence
6	14.8	74.0	84	6	AR052216 Sequence
7	14.8	74.0	84	6	AR194308 Sequence
8	14.8	74.0	87	6	AR052218 Sequence
9	14.8	74.0	87	6	AR194310 Sequence
10	14.2	71.0	32	6	AX466817 Sequence
11	14.2	71.0	30	6	AR1695 Sequence
12	14.2	71.0	45	6	AR180998 Sequence
13	14.2	71.0	45	6	AR180998 Sequence
14	13.8	69.0	31	6	AX245697 Sequence
15	13.8	69.0	51	6	AR002441 Sequence
16	13.8	69.0	51	6	AX116049 Sequence
17	13.8	69.0	51	6	AX113788 Sequence
18	13.8	69.0	59	6	AX322070 Sequence
19	13.8	69.0	59	6	AX322069 Sequence
20	13.8	69.0	66	6	AX322069 Sequence
21	13.8	69.0	66	6	E06635 Sequence
22	13.8	69.0	66	6	E06644 Sequence
23	13.8	69.0	66	6	E07704 Sequence
24	13.8	69.0	66	6	AX322072 Sequence
25	13.8	69.0	68	6	AX322074 Sequence
26	13.8	69.0	68	6	AX322076 Sequence
27	13.8	69.0	68	6	AX322076 Sequence
28	13.8	69.0	68	6	AX322076 Sequence
29	13.8	69.0	68	6	AX322076 Sequence
30	13.8	69.0	68	6	AX322076 Sequence
31	13.8	69.0	75	6	AX322071 Sequence
32	13.8	69.0	75	6	AX322071 Sequence
33	13.8	69.0	75	6	AX322075 Sequence
34	13.8	69.0	75	6	AX322075 Sequence
35	13.8	69.0	75	6	E06037 Sequence
36	13.8	69.0	75	6	E06038 Sequence
37	13.8	69.0	75	6	E07703 Sequence
38	13.8	69.0	75	6	E07703 Sequence
39	13.8	69.0	75	6	AX322215 Sequence
40	13.6	68.0	28	6	AX322215 Sequence
41	13.6	68.0	30	6	E30036 Sequence
42	13.6	68.0	61	14	AF200198 Sequence
43	13.6	68.0	62	6	A62549 Sequence
44	13.6	68.0	82	6	A62549 Sequence
45	13.6	68.0	89	6	AR074468 Sequence

ALIGNMENTS

RESULT 1

AR052214 LOCUS 78 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 6 from patent US 5830866.

ACCESSION AR052214

VERSION AR052214.1 GI:5975578

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 78)

AUTHORS Redel,E. and Altd,F.

TITLE Corticotropin release inhibiting factor and methods of using same

JOURNAL Patent: US 5830866-A 6 03-NOV-1998;

FEATURES Location/Qualifiers

source 1..78
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BASE COUNT 28 a 12 c 31 g 7 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 78;
Best Local Similarity 94.7%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 19
|||||
Db 19 CAAAGGAGCGGAGAGAG 37

RESULT 2
AR052217 96 bp DNA linear PAT 29-SEP-1999
LOCUS AR052217
DEFINITION Sequence 9 from patent US 5830866.
ACCESSION AR052217
VERSION AR052217.1 GI:5975581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 96)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 9 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..96
/organism="unknown"
BASE COUNT 34 a 18 c 37 g 7 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 96;
Best Local Similarity 94.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 19
|||||
Db 37 CAAAGGAGCGGAGAGAG 55

RESULT 3
AR194309 96 bp DNA linear PAT 20-APR-2002
LOCUS AR194309
DEFINITION Sequence 8 from patent US 6348571.
ACCESSION AR194309
VERSION AR194309.1 GI:20240901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 96)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 6348571-A 8 19-FEB-2002;
FEATURES Location/Qualifiers
source 1..96
/organism="unknown"
BASE COUNT 34 a 18 c 37 g 7 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 96;
Best Local Similarity 94.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 19
|||||
Db 37 CAAAGGAGCGGAGAGAG 55

RESULT 4

AR052213 66 bp DNA linear PAT 29-SEP-1999
LOCUS AR052213
DEFINITION Sequence 5 from patent US 5830866.
ACCESSION AR052213
VERSION AR052213.1 GI:5975577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 66)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 5 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..66
/organism="unknown"
BASE COUNT 22 a 11 c 21 g 12 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 66;
Best Local Similarity 88.9%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 18
|||||
Db 19 CAAAGGAGCGGAGAGAG 36

RESULT 5
AR052215 69 bp DNA linear PAT 29-SEP-1999
LOCUS AR052215
DEFINITION Sequence 7 from patent US 5830866.
ACCESSION AR052215
VERSION AR052215.1 GI:5975579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 69)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..69
/organism="unknown"
BASE COUNT 22 a 11 c 24 g 12 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 69;
Best Local Similarity 88.9%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 18
|||||
Db 19 CAAAGGAGCGGAGAGAG 36

RESULT 6
AR052216 84 bp DNA linear PAT 29-SEP-1999
LOCUS AR052216
DEFINITION Sequence 8 from patent US 5830866.
ACCESSION AR052216
VERSION AR052216.1 GI:5975580
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 84)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 8 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..84

BASE COUNT 27 a 17 c 27 g 13 t
ORIGIN
Query Match 74.0%; Score 14.8; DB 6; Length 84;
Best Local Similarity 88.9%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGAGCAGGAGAGAA 18
DB 37 CAAGAGCAGGAGAGAA 54

RESULT 7
LOCUS AR194308 84 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7 from patent US 6348571.
ACCESSION AR194308
VERSION AR194308.1 GI:20240900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 84)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 6348571-A 7 19-FEB-2002;
FEATURES
source 1..84
location/Qualifiers
BASE COUNT 27 a 17 c 27 g 13 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 84;
Best Local Similarity 88.9%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGAGCAGGAGAGAA 18
DB 37 CAAGAGCAGGAGAGAA 54

RESULT 8
LOCUS AR052218 87 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5830866.
ACCESSION AR052218
VERSION AR052218.1 GI:5975582
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 87)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 10 03-NOV-1998;
FEATURES
source 1..87
location/Qualifiers
BASE COUNT 26 a 17 c 31 g 13 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 87;
Best Local Similarity 88.9%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGAGCAGGAGAGAA 18
DB 37 CAAGAGCAGGAGAGAA 54

RESULT 9
LOCUS AR194310 87 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6348571.
ACCESSION AR194310
VERSION AR194310.1 GI:20240902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 87)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 6348571-A 9 19-FEB-2002;
FEATURES
source 1..87
location/Qualifiers
BASE COUNT 26 a 17 c 31 g 13 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 87;
Best Local Similarity 88.9%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGAGCAGGAGAGAA 18
DB 37 CAAGAGCAGGAGAGAA 54

RESULT 10
LOCUS AX466817/c 22 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 299 from Patent WO0212343.
ACCESSION AX466817
VERSION AX466817.1 GI:21900176
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Szytek,K.A., Padigaru,M., Zephusen,B.D., Baumgartner,J.C., Li,L., Casman,S.J., Vernet,C.A., Ballinger,R.A., Shenoy,S.G., Kekuda,R., Burgess,G.E., Meres,P.S., Grosse,W.M., Alsobrook,J.P., Gorman,L., Larocheille,W.D., Traubier,R.J., Coleman,S.D. and Szekeres,E.S.
TITLE Proteins and nucleic acids encoding g-protein coupled receptors
JOURNAL Patent: WO 0212343-A 299 14-FEB-2002;
FEATURES
source 1..22
location/Qualifiers
BASE COUNT 3 a 7 c 3 g 9 t
ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGAGCAGGAGAGAG 20
DB 22 AAAGAGCAGCCTTAAGAG 4

RESULT 11
LOCUS AB1695 30 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 12 from Patent WO9900517.
ACCESSION AB1695
VERSION AB1695.1 GI:6731830
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30)

LOCUS AR194310 87 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6348571.
ACCESSION AR194310
VERSION AR194310.1 GI:20240902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 87)
AUTHORS Redel,E. and Aird,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 6348571-A 9 19-FEB-2002;
FEATURES
source 1..87
location/Qualifiers
BASE COUNT 26 a 17 c 31 g 13 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 87;
Best Local Similarity 88.9%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGAGCAGGAGAGAA 18
DB 37 CAAGAGCAGGAGAGAA 54

RESULT 10
LOCUS AX466817/c 22 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 299 from Patent WO0212343.
ACCESSION AX466817
VERSION AX466817.1 GI:21900176
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Szytek,K.A., Padigaru,M., Zephusen,B.D., Baumgartner,J.C., Li,L., Casman,S.J., Vernet,C.A., Ballinger,R.A., Shenoy,S.G., Kekuda,R., Burgess,G.E., Meres,P.S., Grosse,W.M., Alsobrook,J.P., Gorman,L., Larocheille,W.D., Traubier,R.J., Coleman,S.D. and Szekeres,E.S.
TITLE Proteins and nucleic acids encoding g-protein coupled receptors
JOURNAL Patent: WO 0212343-A 299 14-FEB-2002;
FEATURES
source 1..22
location/Qualifiers
BASE COUNT 3 a 7 c 3 g 9 t
ORIGIN

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Best Local Similarity 84.2%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGAGCAGGAGAGAG 20
DB 22 AAAGAGCAGCCTTAAGAG 4

RESULT 11
LOCUS AB1695 30 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 12 from Patent WO9900517.
ACCESSION AB1695
VERSION AB1695.1 GI:6731830
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30)

AUTHORS Archer, J. A. and Roland, H. J.
 TITLE BIOSENSOR MATERIALS AND METHODS
 JOURNAL Patent: WO 9900517-A 12 07-JAN-1999;
 FEATURES ARCHER JOHN ANTHONY CHARLES (GB); ROLAND HERVE JACQUINAV (GB)
 SOURCE Location/Qualifiers
 1. 30
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 15 a 6 c 8 g 1 t
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 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAAGAGCAGGAGAGAG 19
 Db 12 CAAAGAGCAGGAGAGAGCAG 30

RESULT 12
 LOCUS AR180998 45 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 14 from patent US 6333168.
 ACCESSION AR180998
 VERSION AR180998.1 GI:20223031
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 45)
 AUTHORS Jessell, T. M., Basler, K. and Yamada, T.
 TITLE Cloning, expression and uses of dorsalin-1
 JOURNAL Patent: US 6333168-A 14 25-DEC-2001;
 FEATURES Location/Qualifiers
 source 1. 45
 /organism="unknown"

BASE COUNT 6 a 14 c 8 g 17 t
 ORIGIN

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 Best Local Similarity 84.2%; Pred. No. 8.6e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAAGAGCAGGAGAGAG 19
 Db 35 CAAAGAGCAGGAGAGAG 17

RESULT 13
 LOCUS F222949S02/c 81 bp DNA linear ROD 05-JUL-2000
 DEFINITION Mus musculus Mtf protein (Mtf) gene, alternative exon 1h.
 ACCESSION AF222950
 VERSION AF222950.1 GI:8917536
 KEYWORDS
 SEGMENT 2 of 11
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 81)
 Hallsson, J. H., Fawor, J., Hoddgkinson, C., Glaser, T., Lamoreux, M. L.,
 Magnusdottir, R., Gunnarsson, G. J., Sweet, H. O., Copeland, N. G.,
 Jenkins, N. A. and Steingrimsdottir, E.
 TITLE Genomic, transcriptional and mutational analysis of the mouse
 microphtalmia locus
 JOURNAL Genetics 155 (1), 291-300 (2000)
 MEDLINE 20253112
 PUBMED 10790403
 REFERENCE 2 (bases 1 to 81)
 Hallsson, J. H., Fawor, J., Hodgkinson, C., Glaser, T., Lamoreux, M. L.,
 Magnusdottir, R., Gunnarsson, G. J., Sweet, H. O., Copeland, N. G.,
 AUTHORS Magnusdottir, R., Gunnarsson, G. J., Sweet, H. O., Copeland, N. G.,

TITLE Jenkins, N. A. and Steingrimsdottir, E.
 JOURNAL Direct Submission
 Submitted (11-JAN-2000) Department of Biochemistry and Molecular
 Biology, University of Iceland, Faculty of Medicine,
 Vatnsmyrarvegur 16, Reykjavik 101, Iceland
 FEATURES Location/Qualifiers
 SOURCE 1. 81
 /organism="Mus musculus"
 /strain="129/Sv"
 /db_xref="taxon:10090"
 exon 1. 72
 /gene="Mtf"
 /note="alternatively spliced"
 /number=1h

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 Best Local Similarity 84.2%; Pred. No. 7.6e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAAGAGCAGGAGAGAG 19
 Db 59 CAAAGAGCAGGAGAGAG 41

RESULT 14
 LOCUS AX249697/c 31 bp DNA linear PAT 28-SEP-2001
 DEFINITION Sequence 1776 from Patent WO0166800.
 ACCESSION AX249697
 VERSION AX249697.1 GI:15864320
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 31)
 Cargill, M., Ireland, J. S. and Lander, E. S.
 TITLE Human single nucleotide polymorphisms
 JOURNAL Patent: WO 0166800-A 1776 13-SEP-2001;
 FEATURES WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
 source 1. 31
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 5 a 9 c 6 g 10 t 1 others
 ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 31;
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 Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGAGCAGGAGAGAG 20
 Db 31 AAAGAGCAGGAGAGAG 13

RESULT 15
 LOCUS AR002441/c 51 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 5 from patent US 5741669.
 ACCESSION AR002441
 VERSION AR002441.1 GI:3963995
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 51)
 Krachko, K. Joanne., Jackson, J. Randolph, Hunter., Johnson, J. Helen.,
 Delmar, E. George. and Kral, R. Marden. Jr.
 TITLE Insecticidally effective peptides
 JOURNAL Patent: US 5741669-A 5 21-APR-1998;


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FEATURES                               Location/Qualifiers
Source                               1. 51
BASE COUNT                          7 a 11 c 11 g 22 t
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Best Local Similarity                88.2%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGGAGCAGGGAAGAAG 19
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Db 47 AAGGAGCAGGGAAGAAG 31

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Search completed: December 21, 2002, 12:57:33
 Job Time : 290.367 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 343.641 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-16

Sequence: 1 GTGGAACATGACCCCTTCAGCGG 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: GenBank:*

2: gb_hg:*

3: gb_in:*

4: gb_ov:*

5: gb_ov:*

6: gb_ov:*

7: gb_ov:*

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10: gb_ov:*

11: gb_ov:*

12: gb_ov:*

13: gb_ov:*

14: gb_ov:*

15: gb_ov:*

16: gb_ov:*

17: gb_ov:*

18: gb_ov:*

19: gb_ov:*

20: gb_ov:*

21: gb_ov:*

22: gb_ov:*

23: gb_ov:*

24: gb_ov:*

25: gb_ov:*

26: gb_ov:*

27: gb_ov:*

28: gb_ov:*

29: gb_ov:*

30: gb_ov:*

31: gb_ov:*

32: gb_ov:*

33: gb_ov:*

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44: gb_ov:*

45: gb_ov:*

Result No.	Score	Query Match	Length	DB ID	Description
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2	15.8	65.8	56	114506	114506 Sequence 14
3	15.6	65.0	35	AR105346	AR105346 Sequence
4	15.6	65.0	35	AX067702	AX067702 Sequence
5	15.6	65.0	42	AX209901	AX209901 Sequence
6	15.4	64.2	23	183647	183647 Sequence 21
7	15.4	64.2	23	183648	183648 Sequence 22
8	15.4	64.2	29	AA8907	AA8907 Sequence 3
9	15.4	64.2	44	AX280264	AX280264 Sequence
10	15.4	64.2	52	AA8906	AA8906 Sequence 2
11	15.4	64.2	60	AS0293	AS0293 Sequence 13
12	15.4	64.2	62	AR100681	AR100681 Sequence
13	15.2	63.3	61	AX270703	AX270703 Sequence
14	15.2	63.3	61	AX272234	AX272234 Sequence
15	15.2	62.5	33	AA9027	AA9027 Sequence 9
16	15.2	62.5	33	AA9029	AA9029 Sequence 11
17	15.2	62.5	34	AR081961	AR081961 Sequence
18	15.2	62.5	47	AR100692	AR100692 Sequence
19	15.2	62.5	63	158639	158639 Sequence 7
20	15.2	62.5	80	158639	158639 Sequence 7
21	15.2	62.5	80	158639	158639 Sequence 7
22	15.2	62.5	90	158639	158639 Sequence 7
23	15.2	62.5	97	AF177699	AF177699 Sequence 29
24	14.8	61.7	31	AB3702	AB3702 Sequence 29
25	14.4	60.0	23	158666	158666 Sequence 34
26	14.4	60.0	26	158661	158661 Sequence 29
27	14.4	60.0	26	158661	158661 Sequence 29
28	14.4	60.0	26	158661	158661 Sequence 29
29	14.4	60.0	26	158661	158661 Sequence 29
30	14.4	60.0	82	AF028334	AF028334 Sequence 2
31	14.4	60.0	82	AF028334	AF028334 Sequence 2
32	14.4	60.0	82	AF028334	AF028334 Sequence 2
33	14.4	60.0	82	AF028334	AF028334 Sequence 2
34	14.4	60.0	82	AF028334	AF028334 Sequence 2
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37	14.2	59.2	23	6	6
38	14.2	59.2	23	6	6
39	14.2	59.2	23	6	6
40	14.2	59.2	23	6	6
41	14.2	59.2	23	6	6
42	14.2	59.2	23	6	6
43	14.2	59.2	23	6	6
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45	14.2	59.2	23	6	6

ALIGNMENTS

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LOCUS 112444

DEFINITION Sequence 14 from patent US 5424413.

ACCESSION 112444

VERSION 112444.1

KEYWORDS GI:909828

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 56)

AUTHORS Hogan, J.J., Arnold, L.J., Nelson, N.C., and Bezerkov, R.

TITLE Branched nucleic acid probes

JOURNAL Patent: US 5424413-A 13-JUN-1995;

FEATURES

Location/Qualifiers

56 bp DNA linear PAT 26-JUN-1995

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ORIGIN
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Best Local Similarity 89.5%; Pred. No. 2.8e+04;
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QY 6 ACATGAGCCCTTCAGCG 24
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Db 35 ACCTAAGCCCTTCAGCG 17

RESULT 2
LOCUS 114506 56 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 14 from patent US 5451503.
ACCESSION 114506
VERSION 114506.1 GI:996989
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
AUTHORS 1 (bases 1 to 56)
Hogan, J.J., Arnold, L.J., Jr., Nelson, N.C. and Bezverkoy, R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 14 19-SEP-1995;
FEATURES
source 1..56
/organism="unknown"
BASE COUNT 13 a 17 c 13 g 13 t
ORIGIN
Query Match 65.8%; Score 15.8; DB 6; Length 56;
Best Local Similarity 89.5%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ACATGAGCCCTTCAGCG 24
||| ||||| ||||| |||||
Db 35 ACCTAAGCCCTTCAGCG 17

RESULT 3
LOCUS ARI05346 35 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 27 from patent US 6096539.
ACCESSION ARI05346
VERSION ARI05346.1 GI:12818943
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
AUTHORS 1 (bases 1 to 35)
Gomes, B., Charles, J., Kasof, G.M. and Prosser, J. Caroline.
TITLE Protein activator of apoptosis
JOURNAL Patent: US 6096539-A 27 01-AUG-2000;
FEATURES
source 1..35
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BASE COUNT 3 a 12 c 12 g 8 t
ORIGIN
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Best Local Similarity 81.8%; Pred. No. 3.8e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGACATGAAGCCCTTCAGCG 24
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Db 35 GGACACCAAGCTCTTAAGCG 14

RESULT 4

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AX067702/c AX067702 35 bp DNA linear PAT 19-JAN-2001
LOCUS
DEFINITION Sequence 27 from Patent WO0077200.
ACCESSION AX067702
VERSION AX067702.1 GI:12329589
KEYWORDS
SOURCE
ORGANISM
REFERENCE
synthetic construct.
AUTHORS 1 (bases 1 to 35)
Gomes, B.C., Kasof, G.M. and Prosser, J.C.
TITLE Receptor interacting protein r193
JOURNAL Patent: WO 0077200-A 27 21-DEC-2000;
Astrazeneca AB (SE)
FEATURES
source 1..35
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 3 a 12 c 12 g 8 t
ORIGIN
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Best Local Similarity 81.8%; Pred. No. 3.8e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGACATGAAGCCCTTCAGCG 24
||||| ||| ||||| |||||
Db 35 GGACACCAAGCTCTTAAGCG 14

RESULT 5
LOCUS AX209901 42 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 3 from Patent WO0157240.
ACCESSION AX209901
VERSION AX209901.1 GI:15424322
KEYWORDS
SOURCE
ORGANISM
REFERENCE
synthetic construct.
AUTHORS 1 (bases 1 to 42)
Melcher, T. and Kask, R.
TITLE Interaction of mdma receptor with protein tyrosine phosphatase
JOURNAL Patent: WO 0157240-A 3 09-AUG-2001;
Agy Therapeutics, Inc. (US)
FEATURES
source 1..42
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="antisense oligonucleotide"
BASE COUNT 9 a 19 c 6 g 8 t
ORIGIN
Query Match 65.0%; Score 15.6; DB 6; Length 42;
Best Local Similarity 81.8%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGACATGAAGCCCTTCAGCG 24
||||| ||| ||||| |||||
Db 10 GCACACGAAGCCCTTCAGCTG 31

RESULT 6
LOCUS I83647 23 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 21 from patent US 5714583.
ACCESSION I83647
VERSION I83647.1 GI:3407177
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.

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Matches	10	Conserved	10
QY	8	ATGAGCCCTCAGCG	2
DB	18	ATGAGCCCTCAGCG	2

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RESULT 11
A50293          60 bp   DNA      linear   PAT 07-MAR-1997
DEFINITION      Sequence 13 from Patent WO9612803.
ACCESSION       A50293
VERSION         A50293.1 GI:2303347
KEYWORDS
SOURCE          unidentified.
ORGANISM        unidentified.
REFERENCE       1 (bases 1 to 60)
AUTHORS        Blumenfeld,M.
TITLE          METHOD FOR THE EX VIVO TREATMENT OF TUMOUR CELLS FROM PATIENTS WITH
JOURNAL        CM
COMMENT         Patent: WO 9612803-A 13 02-MAY-1996;
FEATURES        Other publication FR 2726004 960426.
SOURCE          1..60
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                /db_xref="taxon:32644"
BASE COUNT      18 a 18 c 13 g 11 t
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Best Local Similarity 94.1%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCCTTCAGCG 24
Db 28 AAGAAGCCCTTCAGCG 44

RESULT 12
A100681         62 bp   DNA      linear   PAT 14-FEB-2001
DEFINITION      Sequence 1 from patent US 6080851.
ACCESSION       A100681
VERSION         A100681.1 GI:12811129
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 62)
AUTHORS        Pachuk,C.J.; Coney,L.R. and Oakes,F.T.
TITLE          Ribozymes with linked anchor sequences
JOURNAL        Patent: US 6080851-A 1 27-JUN-2000;
FEATURES        Location/Qualifiers
SOURCE          1..62
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BASE COUNT      18 a 19 c 13 g 12 t
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Query Match     64.2%; Score 15.4; DB 6; Length 62;
Best Local Similarity 94.1%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCCTTCAGCG 24
Db 29 AAGAAGCCCTTCAGCG 45

RESULT 13
AX270703        61 bp   DNA      linear   PAT 29-OCT-2001
DEFINITION      Sequence 1334 from Patent WO0164876.
ACCESSION       AX270703
VERSION         AX270703.1 GI:16543479
KEYWORDS
SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
                /organism="unidentified"
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REFERENCE       1
AUTHORS        Stefansson,H., Steinhorsdottir,V. and Gulcher,J.R.
TITLE          Human schizophrenia gene
JOURNAL        Patent: WO 0164876-A 1334 07-SEP-2001;
FEATURES        Decode Genetics EHF. (IS)
SOURCE          Location/Qualifiers
                1..61
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
BASE COUNT      25 a 6 c 9 g 20 t 1 others
ORIGIN
Query Match     63.3%; Score 15.2; DB 6; Length 61;
Best Local Similarity 85.0%; Pred. No. 5.3e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACATGAGCCCTTCAG 21
Db 37 TGGATATGAGCATTTTCAG 56

RESULT 14
AX272234        61 bp   DNA      linear   PAT 29-OCT-2001
LOCUS          AX272234
DEFINITION      Sequence 1334 from Patent WO0164877.
ACCESSION       AX272234
VERSION         AX272234.1 GI:16544971
KEYWORDS
SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS        Stefansson,H., Steinhorsdottir,V. and Gulcher,J.R.
TITLE          Human schizophrenia gene
JOURNAL        Patent: WO 0164877-A 1334 07-SEP-2001;
FEATURES        Decode Genetics EHF. (IS)
SOURCE          Location/Qualifiers
                1..61
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
BASE COUNT      25 a 6 c 9 g 20 t 1 others
ORIGIN
Query Match     63.3%; Score 15.2; DB 6; Length 61;
Best Local Similarity 85.0%; Pred. No. 5.3e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACATGAGCCCTTCAG 21
Db 37 TGGATATGAGCATTTTCAG 56

RESULT 15
A49027          33 bp   DNA      linear   PAT 07-MAR-1997
DEFINITION      Sequence 9 from Patent WO9606166.
ACCESSION       A49027
VERSION         A49027.1 GI:2302637
KEYWORDS
SOURCE          unidentified.
ORGANISM        unidentified.
REFERENCE       1 (bases 1 to 33)
AUTHORS        Choo,Y., Kling,A. and Garcia,I.
TITLE          IMPROVEMENTS IN OR RELATING TO BINDING PROTEINS FOR RECOGNITION OF
JOURNAL        DNA
COMMENT         Patent: WO 9606166-A 9 29-FEB-1996;
FEATURES        MEDICAL RES COUNCIL (GB)
                Other publication AU 3229195 960314.
                Location/Qualifiers
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Query Match 62.5%; Score 15; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.1e+04;
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 Db 16 GAAGCCCTTCAGCG 30

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7

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score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using SW model

2032.551 million cell updates/sec

Sequence: 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27

SCORING: IDENT111=NO
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

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Minimum DB seq length: 0
Maximum DB seq length: 100
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Post-processing:	Minimum Match 0%
	Maximum Match 100%

Listing first 45 summaries

Database :

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34: em.hrg.pln.*
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40: em.hrgo.mus.*
41: em.hrgo.other.*

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Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	ID	Description
1	26	96.3	80	6	I58639 Sequence 7
2	26	96.3	80	6	I96201 Sequence 38
3	22	81.5	22	6	AR086401 Sequence
4	22	81.5	22	6	I44731 Sequence 10
5	22	81.5	22	6	I92877 Sequence 1
6	19	70.4	24	6	E16995 Primer. 7/1
7	19	70.4	24	6	E93183 Sequence 6
8	18	66.7	69	6	AX13191 Sequence 14
9	17	63.0	51	6	AX115325 Sequence
10	17	63.0	56	6	I12449 Sequence 19
11	17	63.0	56	6	I14511 Sequence 19
12	17	63.0	68	6	A63190 Sequence 13
13	17	63.0	76	3	SODIRLXY06
14	17	63.0	76	3	SODIRLXY02
15	16.8	62.2	71	9	HSAL6SN
16	16.4	60.7	28	6	E26953
17	16	59.3	10	6	AF224105
18	16	59.3	67	6	A93189
19	16	59.3	75	9	FL185592S11
20	15.8	58.5	20	6	I23911
21	15.6	57.8	29	6	I27229 Sequence 35
22	15.2	56.3	29	6	A56950 Sequence 8
23	15.2	56.3	61	4	AX204128
24	15.2	56.3	54	6	F292317S02
25	15	55.6	16	6	E13680
26	15	55.6	20	6	AR037942
27	15	55.6	40	6	AR037936
28	15	55.6	40	6	AR037937
29	15	55.6	66	6	A93188
30	14.8	54.8	24	6	AX443608
31	14.8	54.8	25	6	AX447590
32	14.8	54.8	64	6	AX14972
33	14.8	54.8	67	6	AX336630
34	14.8	54.8	69	6	MSU09943
35	14.8	54.8	69	6	AX435653
36	14.8	54.8	69	6	AX435678
37	14.8	54.8	76	1	BSRNMK
38	14.8	54.8	76	6	AX435559
39	14.8	54.8	76	6	AX435699
40	14.8	54.8	76	6	AX436011
41	14.8	54.8	76	6	AX436029
42	14.8	54.8	76	6	AX439994
43	14.8	54.8	76	6	AX440034
44	14.8	54.8	76	6	AX440046
45	14.8	54.8	76	6	AX440062
					Sequence

ALIGNMENTS

RESULT 1			
LOCUS	I58639		
DEFINITION	Sequence 7 from patent US 5652222.	80 bp	DNA
ACCESSION	I58639		Linear
VERSION	I58639.1		PAT 07-OCT-1997
KEYWORDS	GI:2477877		
SOURCE	unknown.		
ORGANISM	unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 80)		
TITLE	Calabretta,B. and Gewirtz,A.M. Selective inhibition of leukemic cell proliferation by bcr-abl antisense oligonucleotides		
JOURNAL	Patent: US 5652222-A 7 29-JUL-1997;		

FEATURES Location/Qualifiers
 source 1..80
 /organism="unknown"
 BASE COUNT 16 a 22 c 27 g 15 t
 ORIGIN

Query Match 96.3%; Score 26; DB 6; Length 80;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
 |||
 Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 2
 LOCUS 196201 80 bp DNA linear PAT 01-DEC-1998
 DEFINITION Sequence 38 from patent US 5734039.
 ACCESSION 196201
 VERSION 196201.1 GI:3940671
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 80)
 AUTHORS Calabretta, B. and Skorski, T.
 TITLE Antisense oligonucleotides targeting cooperating oncogenes
 JOURNAL Patent: US 5734039-A 38 31-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..80
 /organism="unknown"

BASE COUNT 16 a 22 c 27 g 15 t
 ORIGIN

Query Match 96.3%; Score 26; DB 6; Length 80;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
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 Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 3
 LOCUS AR086401/c 22 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 1 from patent US 5985572.
 ACCESSION AR086401
 VERSION AR086401.1 GI:10013167
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Macfarlane, D.E.
 TITLE Quaternary amine surfactant and methods of using same in isolation
 JOURNAL Patent: US 5985572-A 1 16-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..22
 /organism="unknown"

BASE COUNT 6 a 7 c 5 g 4 t
 ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGA 25
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 Db 22 GACTTTGAGCCTCAGGCTCTGA 1

RESULT 4
 LOCUS I44731/c 22 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 10 from patent US 5635385.
 ACCESSION I44731
 VERSION I44731.1 GI:2469444
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Leopold, L.H., Shore, S.K., Reddy, M.V.R. and Reddy, E.Premkumar.
 TITLE Multi-unit ribozyme inhibition of oncogene gene expression
 JOURNAL Patent: US 5635385-A 10 03-JUN-1997;
 FEATURES Location/Qualifiers
 source 1..22
 /organism="unknown"

BASE COUNT 6 a 7 c 5 g 4 t
 ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGA 25
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 Db 22 GACTTTGAGCCTCAGGCTCTGA 1

RESULT 5
 LOCUS I92877/c 22 bp DNA linear PAT 01-DEC-1998
 DEFINITION Sequence 1 from patent US 5728822.
 ACCESSION I92877
 VERSION I92877.1 GI:3937347
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Macfarlane, D.E.
 TITLE Quaternary amine surfactants and methods of using same in isolation
 JOURNAL Patent: US 5728822-A 1 17-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..22
 /organism="unknown"

BASE COUNT 6 a 7 c 5 g 4 t
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Query Match 81.5%; Score 22; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGA 25
 |||
 Db 22 GACTTTGAGCCTCAGGCTCTGA 1

RESULT 6
 LOCUS E16995 24 bp DNA linear PAT 28-JUL-1999
 DEFINITION Primer.
 ACCESSION E16995
 VERSION E16995.1 GI:5711678
 KEYWORDS JP 1998229899-A/10.
 SOURCE unidentified.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Kobayashi, M., Kawaguchi, R., Segawa, M. and Takarada, Y.
 TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA, AND

JOURNAL
DETECTION OF BCR/ABL TYPE CHIMERA MESSENGER RNA AND USING THE SAME
Patent: JP 199822899-A 10 02-SEP-1998;
S R I.KK. TOYORO CO LTD

COMMENT

OS None
OC Artificial sequences.
PN JP 199822899-A/10
PD 02-SEP-1998 JP 1997054092
PI KOHAYASHI MASARU, KAMAGUCHI RYUJI, SEGAWA MASAYA, PI
TAKARADA YUTAKA
PC C1201/68,G01N33/50//C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key
FH location: location/Qualifiers
FT source 1. .24
location/Qualifiers
/organism="Artificial sequences".

FEATURES

source
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/db_xref="taxon:32644"

BASE COUNT

5 a 6 c 6 g 7 t

ORIGIN

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCTTCAGG 19
|||||
Db 6 TCTGACTTTGAGCTTCAGG 24

RESULT 7
A93183/c A93183 70 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 6 from Patent WO9746672.
DEFINITION A93183
ACCESSION A93183
VERSION A93183.1 GI:6741568
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 70)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL PATENT: WO 9746672-A 6 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES

source
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/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 15 a 18 c 22 g 15 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCTTCAGG 19
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Db 19 TCTGACTTTGAGCTTCAGG 1

RESULT 8
A93191/c A93191 69 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 14 from Patent WO9746672.
DEFINITION A93191
ACCESSION A93191
VERSION A93191.1 GI:6741576
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified

REFERENCE 1 (bases 1 to 69)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL PATENT: WO 9746672-A 14 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES

source
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/db_xref="taxon:32644"

BASE COUNT 15 a 17 c 22 g 15 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCTTCAG 18
|||||
Db 18 TCTGACTTTGAGCTTCAG 1

RESULT 9
AX115325 AX115325 51 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 448 from Patent WO0129262.
DEFINITION AX115325
ACCESSION AX115325
VERSION AX115325.1 GI:14032267
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 51)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL PATENT: WO 0129262-A 448 26-APR-2001;
Orchid Biosciences, Inc. (US)

FEATURES

source
1. .51
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 5 c 21 g 19 t

ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 TGACTTTGAGCTTCAGGCTGTGAGT 27
|||||
Db 11 TGACTTTGAGCTTCAGGCTGTGAGT 35

RESULT 10
112449 112449 56 bp DNA linear PAT 26-JUL-1995
LOCUS Sequence 19 from patent US 5424413.
DEFINITION 112449
ACCESSION 112449
VERSION 112449.1 GI:909833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.V., Arnold,L.J. Jr., Nelson,N.C. and Bezerkov,R.
TITLE Branched nucleic acid probes
JOURNAL PATENT: US 5424413-A 19 13-JUN-1995;
Location/Qualifiers

FEATURES
source
1. .56
/organism="unknown"
BASE COUNT 13 a 14 c 15 g 14 t

ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0;

QY 1 TCTGACTTGAGCCTCA 17
|||||
Db 40 TCTGACTTGAGCCTCA 56

RESULT 11

LOCUS 114511 56 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 19 from patent US 5451503.
ACCESSION 114511
VERSION 114511.1 GI:996994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J., Jr., Nelson,N.C. and Bezverkov,R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 19 19-SEP-1995;
FEATURES Location/Qualifiers
source 1..56
/organism="unknown"

BASE COUNT 13 a 14 c 15 g 14 t
ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
|||||
Db 40 TCTGACTTGAGCCTCA 56

RESULT 12

LOCUS A93190 68 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 13 from Patent WO9746672.
ACCESSION A93190
VERSION A93190.1 GI:6741575
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 68)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 13 11-DEC-1997;
FEATURES DEUTSCHES KREBSFORSCH (DE); SCZAKIEL, GEORG (DE)
source 1..68
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 15 a 16 c 22 g 15 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
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Db 17 TCTGACTTGAGCCTCA 1

RESULT 13
SODTRLXS06 76 bp tRNA linear INV 04-NOV-1999
LOCUS SODTRLXS06

DEFINITION Squid tRNA-Lys(UUU).
ACCESSION D50539
VERSION D50539.1 GI:1256933
KEYWORDS tRNA-Lys.
SOURCE Loligo bleekeri tRNA.
ORGANISM Loligo bleekeri

REFERENCE 1 (bases 1 to 76)
AUTHORS Matsuo,M., Abe,Y., Saruta,Y. and Okada,N.
TITLE Mollusk genes encoding lysine tRNA (UUU) contain introns
JOURNAL Gene 165 (2), 249-253 (1995)
MEDLINE 96096530
REFERENCE 2 (bases 1 to 76)
AUTHORS Matsuo,M.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1995) Mami Matsuo, Tokyo Institute of Technology,
Faculty of Bioscience and Biotechnology; Nagatsuta 4259, Yokohama,
Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)
Location/Qualifiers

FEATURES

source

trna

modified_base

modified_base

modified_base

modified_base

modified_base

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modified_base

modified_base

BASE COUNT 14 a 20 c 22 g 19 t 1 others
ORIGIN

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Best Local Similarity 76.9%; Pred. No. 3.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCGACGGCTGTGAG 26
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Db 27 TCAGACTTTTANCTGAGGCTCTGGG 52

RESULT 14
SODTRLXS2 76 bp tRNA linear INV 04-NOV-1999
LOCUS SODTRLXS2
DEFINITION Loligo bleekeri tRNA-Lys.
ACCESSION D45191
VERSION D45191.1 GI:1065614

KEYWORDS tRNA-Lys.
SOURCE Loligo bleekeri tRNA.
ORGANISM Loligo bleekeri
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoida;
Mysidota; Loliginidae; Loligo.
AUTHORS Matsuo, M., Yokogawa, T., Nishikawa, K., Watanabe, K. and Okada, N.
TITLE Highly specific and efficient cleavage of squid tRNA(Lys) catalyzed by magnesium ions
JOURNAL J. Biol. Chem. 270 (17), 10097-10104 (1995)
MEDLINE 95247717
REFERENCE 2 (bases 1 to 76)
AUTHORS Matsuo, M.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1995) Mam1 Matsuo, Tokyo Institute of Technology, Faculty of Bioscience and Biotechnology; Nagatsuta 4259, Yokohama, Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)
LOCATION/Qualifiers
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/db_xref="taxon:6617"
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/product="tRNA-Lys"
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modified_base /mod_base=m2g
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modified_base /note="derivative of U"
37
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ORIGIN
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Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 TCTGACTTGGAGCTCAGGCTGAG 26
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DB 27 TCAGACTTTTANCTGAGGCTCTGG 52

RESULT 15
LOCUS HSA16SN 71 bp mRNA linear PRI 07-MAY-1999
DEFINITION H.sapiens mRNA for U56 small nuclear RNA.
ACCESSION X96653.1
VERSION X96653.1 GI:1321840
KEYWORDS small nuclear RNA.
SOURCE Homo sapiens.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Kiss-Laszlo, Z., Henry, Y., Bachellerie, J.P., Caizergues-Ferrer, M.
TITLE Site-specific ribose methylation of preribosomal RNA: a novel function for small nuclear RNAs
JOURNAL Cell 85 (7), 1077-1088 (1996)
MEDLINE 96270510
PUBMED 8674114
REFERENCE 2 (bases 1 to 71)
AUTHORS Kiss, T.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) T. Kiss, Iab. Biol. Mol. Euc. du CNRS, Universit. Paul Sabatier, 118, route de Narbonne, 31062 Toulouse Cedex, France
LOCATION/Qualifiers
FEATURES
source 1..71
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"
/note="C and D boxes"
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/gene="U56 small nuclear RNA"
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/gene="U56 small nuclear RNA"
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BASE COUNT 18 a 14 c 18 g 21 t
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Best Local Similarity 90.0%; Pred. No. 4.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 TTGAGCTCAGGCTCTGAGT 27
||||| ||| ||||| |||
DB 50 TTGAGACTCTGGGCTCTGAGT 69

Search completed: December 21, 2002, 12:57:42
Job time : 391.596 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 : Search time 386.596 Seconds

(Without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 27

Sequence: 1 UCUGACUUGAGCCUCAGGUCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: gb_hlg:*
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13: gb_un:*
14: gb_vl:*
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41: em_hlg_others:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	96.3	80	6	158639
2	26	96.3	80	6	196201
3	22	81.5	22	6	AR086401
4	22	81.5	22	6	144731
5	22	81.5	22	6	192877
6	19	70.4	24	6	E16995
7	19	70.4	20	6	A93183
8	17	63.0	69	6	A93191
9	17	63.0	51	6	AX115325
10	17	63.0	56	6	112449
11	17	63.0	56	6	114511
12	17	63.0	68	6	A93190
13	17	63.0	76	3	SQPRRYXS06
14	17	63.0	76	3	SQPRRYXS2
15	16.8	62.2	71	9	HSR16SN
16	16.4	60.7	28	6	E26953
17	16	59.3	54	10	AF224105
18	16	59.3	67	6	A93189
19	16	59.3	75	9	F185592S11
20	15.8	58.5	20	6	123911
21	15.8	57.8	67	6	127229
22	15.2	56.3	29	6	A56950
23	15.2	56.3	51	6	AX204128
24	15.2	56.3	64	4	F292317S02
25	15.2	55.6	16	6	E13680
26	15	55.6	20	6	AR037942
27	15	55.6	40	6	AR037936
28	15	55.6	40	6	AR037937
29	15	55.6	66	6	A93188
30	14.8	54.8	24	6	AX443608
31	14.8	54.8	25	6	AX447590
32	14.8	54.8	64	6	AX436030
33	14.8	54.8	67	5	MSU09943
34	14.8	54.8	69	5	AX435963
35	14.8	54.8	69	6	AX435978
36	14.8	54.8	76	1	BSRNK
37	14.8	54.8	76	6	AX435959
38	14.8	54.8	76	6	AX435999
39	14.8	54.8	76	6	AX436011
40	14.8	54.8	76	6	AX436029
41	14.8	54.8	76	6	AX439994
42	14.8	54.8	76	6	AX440034
43	14.8	54.8	76	6	AX440046
44	14.8	54.8	76	6	AX440062
45	14.8	54.8	76	6	AX440062

ALIGNMENTS

RESULT 1
LOCUS 158639
DEFINITION Sequence 7 from patent US 5652222.
ACCESSION 158639
VERSION 158639.1 GI:2477877
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 80)
AUTHORS Calabretta, B. and Gewirtz, A.M.
TITLE Selective inhibition of leukemic cell proliferation by bcr-abl antisense oligonucleotides
JOURNAL Patent: US 5652222-A 7 29-JUL-1997;

80 bp. DNA linear PAT 07-OCT-1997

FEATURES Location/Qualifiers
 source 1..80
 BASE COUNT 16 a 22 c 27 g 15 t
 ORIGIN

Query Match 96.3%; Score 26; DB 6; Length 80;
 Best Local Similarity 69.2%; Pred. No. 0.21;
 Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUGAGCCUCAGGUCUGAG 26
 Db 55 TCTGACTTGGAGCCTCAGGGTCTGAG 80

RESULT 2
 LOCUS 196201
 DEFINITION Sequence 38 from patent US 5734039.
 ACCESSION 196201
 VERSION 196201.1 GI:3940671
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 80)
 AUTHORS Calabretta,B. and Skorski,T.
 TITLE Antisense oligonucleotides targeting cooperating oncogenes
 JOURNAL Patent: US 5734039-A 38 31-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..80
 BASE COUNT 16 a 22 c 27 g 15 t
 ORIGIN

Query Match 96.3%; Score 26; DB 6; Length 80;
 Best Local Similarity 69.2%; Pred. No. 0.21;
 Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUGAGCCUCAGGUCUGAG 26
 Db 55 TCTGACTTGGAGCCTCAGGGTCTGAG 80

RESULT 3
 LOCUS AR086401/c
 DEFINITION Sequence 1 from patent US 5985572.
 ACCESSION AR086401
 VERSION AR086401.1 GI:10013167
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Macfarlane,D.E.
 TITLE Quaternary amine surfactant and methods of using same in isolation of RNA
 JOURNAL Patent: US 5985572-A 1 16-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..22
 BASE COUNT 6 a 7 c 5 g 4 t
 ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
 Best Local Similarity 72.7%; Pred. No. 17;
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUGAGCCUCAGGUCUGA 25
 Db 22 GACTTTGAGCCTCAGGGTCTGA 1

RESULT 4
 LOCUS I44731/c
 DEFINITION Sequence 10 from patent US 5635385.
 ACCESSION I44731
 VERSION I44731.1 GI:2469444
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Leopold,L.H., Shore,S.K., Reddy,M.V.R. and Reddy,E.Premkumar.
 TITLE Multi-unit ribozyme inhibition of oncogene gene expression
 JOURNAL Patent: US 5635385-A 10 03-JUN-1997;
 FEATURES Location/Qualifiers
 source 1..22
 BASE COUNT 6 a 7 c 5 g 4 t
 ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
 Best Local Similarity 72.7%; Pred. No. 17;
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUGAGCCUCAGGUCUGA 25
 Db 22 GACTTTGAGCCTCAGGGTCTGA 1

RESULT 5
 LOCUS I92877/c
 DEFINITION Sequence 1 from patent US 5728822.
 ACCESSION I92877
 VERSION I92877.1 GI:3937347
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Macfarlane,D.E.
 TITLE Quaternary amine surfactants and methods of using same in isolation of RNA
 JOURNAL Patent: US 5728822-A 1 17-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..22
 BASE COUNT 6 a 7 c 5 g 4 t
 ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
 Best Local Similarity 72.7%; Pred. No. 17;
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUGAGCCUCAGGUCUGA 25
 Db 22 GACTTTGAGCCTCAGGGTCTGA 1

RESULT 6
 LOCUS E16995
 DEFINITION Primer.
 ACCESSION E16995
 VERSION E16995.1 GI:5711678
 KEYWORDS JP 1988229899-A/10.
 SOURCE unidentified.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Kobayashi,M., Kawaguchi,R., Segawa,M. and Takarada,Y.
 TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA, AND

JOURNAL
DETECTION OF BCR/ABL TYPE CHIMERA MESSENGER RNA AND USING THE SAME
Patent: JP 1998229899-A 10 02-SEP-1998;
S R I:KK, TOYOBO CO LTD
COMMENT
OS None
OC Artificial sequences.
PN JP 1998229899-A/10
PD 02-SEP-1998
PF 21-FEB-1997 JP 1997054092
PI KOBAYASHI MASARU, KAWAGUCHI RYUJI, SEGAWA MASAYA, PI
TAKARADA YUTAKA
PC C1201/68, G01N33/50//C12N15/09;
CC strandedness: Single;
FH topology: Linear;
FH key Location/Qualifiers
FT source 1. 24
FEATURES
source Location/Qualifiers
1. 24
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/db_xref="taxon:32644"
BASE COUNT 5 a 6 c 6 g 7 t
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Best Local Similarity 68.4%; Pred. No. 4.2e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
OY 1 UCUGACUUUGAGCCUCAG 19
Db 6 TCTGACTTGTGAGCCTCAG 24
RESULT 7
A93183/C A93183 70 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 6 from Patent WO9746672.
DEFINITION A93183
ACCESSION A93183 GI:6741568
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 70)
AUTHORS Sczakiel, G. and Haas, R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 6 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
FEATURES
source 1. 70
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 15 a 18 c 22 g 15 t
ORIGIN
Query Match 70.4%; Score 19; DB 6; Length 70;
Best Local Similarity 68.4%; Pred. No. 4.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
OY 1 UCUGACUUUGAGCCUCAG 19
Db 19 TCTGACTTGTGAGCCTCAG 1
RESULT 8
A93191/C A93191 69 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 14 from Patent WO9746672.
DEFINITION A93191
ACCESSION A93191 GI:6741576
VERSION
KEYWORDS
SOURCE
ORGANISM
unidentified.
unidentified.

unclassified.
REFERENCE 1 (bases 1 to 69)
AUTHORS Sczakiel, G. and Haas, R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 14 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
FEATURES
source 1. 69
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 15 a 17 c 22 g 15 t
ORIGIN
Query Match 66.7%; Score 18; DB 6; Length 69;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
OY 1 UCUGACUUUGAGCCUCAG 18
Db 18 TCTGACTTGTGAGCCTCAG 1
RESULT 9
AX115325 AX115325 51 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 448 from Patent WO0129262.
DEFINITION AX115325
ACCESSION AX115325 GI:14032267
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Picoult-Newbury, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 448 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source 1. 51
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 6 a 5 c 21 g 19 t
ORIGIN
Query Match 63.0%; Score 17; DB 6; Length 51;
Best Local Similarity 48.0%; Pred. No. 3.6e+03;
Matches 12; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
OY 3 UCAGUUUGAGCCUCAGGUCUGAGU 27
Db 11 TGACTTGTGAGTCAGTCGTGTGT 35
RESULT 10
112449 112449 56 bp DNA linear PAT 26-JUL-1995
LOCUS Sequence 19 from patent US 5424413.
DEFINITION 112449
ACCESSION 112449 GI:909833
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 56)
AUTHORS Hogan, J.J., Arnold, L.J. Jr., Nelson, N.C. and Beazekov, R.
TITLE Branched nucleic acid probes
JOURNAL Patent: US 5424413-A 19 13-JUN-1995;
LOCATION/Qualifiers
source 1. 56
/organism="unknown"
BASE COUNT 13 a 14 c 15 g 14 t
ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 56;
Best Local Similarity 64.7%; Pred. No. 3.6e+03;
Matches 11; Conservative 6; Mismatches 0; Indels 0;

QY 1 UCUGACUUUGAGCCUCA 17
Db 40 TCTGACTTTGAGCCTCA 56
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RESULT 11

LOCUS 114511 56 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 19 from patent US 5451503.
ACCESSION 114511
VERSION 114511.1 GI:996994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan, J.J., Arnold, L.J., Jr., Nelson, N.C. and Bezverkov, R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 19 19-SEP-1995;
FEATURES
Location/Qualifiers
Source 1..56
/organism="unknown"

BASE COUNT 13 a 14 c 15 g 14 t
ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 56;
Best Local Similarity 64.7%; Pred. No. 3.6e+03;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCA 17
Db 40 TCTGACTTTGAGCCTCA 56
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RESULT 12

LOCUS A93190 68 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 13 from Patent WO9746672.
ACCESSION A93190
VERSION A93190.1 GI:6741575
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 68)
AUTHORS Sczakiel, G. and Haas, R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 13 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SZAKIEL GEORG (DE)
FEATURES
Location/Qualifiers
Source 1..68
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 15 a 16 c 22 g 15 t
ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 68;
Best Local Similarity 64.7%; Pred. No. 3.5e+03;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCA 17
Db 17 TCTGACTTTGAGCCTCA 1
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RESULT 13
LOCUS SODTRLYS06 76 bp tRNA linear INV 04-NOV-1999
SODTRLYS06

DEFINITION Squid tRNA-Lys(UUU).
ACCESSION D50539
VERSION D50539.1 GI:1256933
KEYWORDS tRNA-Lys.
SOURCE Loligo bleekeri tRNA.
ORGANISM Loligo bleekeri
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
Myopsida; Loliginidae; Loligo.

REFERENCE 1 (bases 1 to 76)
AUTHORS Matsuo, M., Abe, Y., Saruta, Y. and Okada, N.
TITLE Mollusk genes encoding lysine tRNA (UUU) contain introns
JOURNAL Gene 165 (2), 249-253 (1995)
MEDLINE 96096530
REFERENCE 2 (bases 1 to 76)
AUTHORS Matsuo, M.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1995) Mami Matsuo, Tokyo Institute of Technology,
Faculty of Bioscience and Biotechnology, Nagatsuta 4259, Yokohama,
Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)

FEATURES

source
Location/Qualifiers
1..76
/organism="Loligo bleekeri"
/db_xref="taxon:6617"
1..76
/product="tRNA-Lys"
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/anticodon="(pos:34..36,aa:Lys)"
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/mod_base=m2g
16
/mod_base=d
27
/mod_base=p
34
/note="unidentified modified nucleotide"
/mod_base=OTHER
37
/note="unidentified modified nucleotide"
/mod_base=OTHER
46
/mod_base=m7g
47
/mod_base=d
48
/mod_base=m5c
54
/mod_base=tm
55
/mod_base=p
58
/mod_base=m1a
67
/mod_base=m2g
72
/mod_base=m5c
20 c 22 g 19 t 1 others

BASE COUNT 14 a 20 c 22 g 19 t 1 others
ORIGIN

Query Match 63.0%; Score 17; DB 3; Length 76;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUGAG 26
Db 27 TCAGACTTTTANCTGAGGCTGTGG 52
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RESULT 14
LOCUS SODTRLYS2 76 bp tRNA linear INV 04-NOV-1999
DEFINITION Loligo bleekeri tRNA-Lys.
ACCESSION D45191
VERSION D45191.1 GI:1065614

KEYWORDS trna-lys.
SOURCE Loligo bleekeri trna.
ORGANISM Loligo bleekeri
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
Mysidacea; Loliginidae; Loligo.
REFERENCE Matsuo, M., Yokogawa, T., Nishikawa, K., Watanabe, K. and Okada, N.
AUTHORS 1 (bases 1 to 76)
TITLE Highly specific and efficient cleavage of squid trna(lys) catalyzed
by magnesium ions
JOURNAL J. Biol. Chem. 270 (17), 10097-10104 (1995)
MEDLINE 95247717
REFERENCE 2 (bases 1 to 76)
AUTHORS Matsuo, M.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1995) Mami Matsuo, Tokyo Institute of Technology,
Faculty of Bioscience and Biotechnology; Nagatsuta 4259, Yokohama,
Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)
LOCATION/Qualifiers
FEATURES
source 1..76
/organism="Loligo bleekeri"
/db_xref="taxon:6617"
1..76
/product="trna-lys"
/note="Codon recognized: AAA"
/anticodon=(pos:34..36,aa:lys)
10
/mod_base=m2g
16
/mod_base=d
27
/mod_base=p
34
/note="derivative of u"
/mod_base=OTHER
37
/note="derivative of A"
/mod_base=OTHER
46
/mod_base=m7g
47
/mod_base=d
48
/mod_base=m5c
54
/mod_base=tm
55
/mod_base=p
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67
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72
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BASH COUNT 14 a 20 c 22 g 19 t 1 others
ORIGIN
Query Match 63.0%; Score 17; DB 3; Length 76;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 UCUGACUUGAGCCUCAGGUCUGAG 26
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Db 27 TCAGACTTTTAACTGAGGCTGCGG 52

RESULT 15
LOCUS HSA16SN 71 bp mRNA linear PRI 07-MAY-1999
DEFINITION H.sapiens mRNA for U56 small nuclear RNA.
ACCESSION X96655
VERSION X96655.1 GI:1321840
KEYWORDS small nuclear RNA.
SOURCE Homo sapiens.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Kiss, T., Henry, Y., Bachelier, J.P., Calzergues-Ferrer, N.
AUTHORS 1 (bases 1 to 71)
TITLE Site-specific ribose methylation of preribosomal RNAs: a novel
function for small nuclear RNAs
JOURNAL Cell 85 (7), 1077-1088 (1996)
MEDLINE 8674114
REFERENCE 2 (bases 1 to 71)
AUTHORS Kiss, T.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) T. Kiss, Lab. Biol. Mol. Euc. du CNRS,
Universit Paul Sabatier, 118, route de Narbonne, 31062 Toulouse
Cedex, France
LOCATION/Qualifiers
FEATURES
source 1..71
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"
/note="C and D boxes"
1..71
/gene="U56 small nuclear RNA"
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/gene="U56 small nuclear RNA"
BASH COUNT 18 a 14 c 18 g 21 t
ORIGIN
Query Match 62.2%; Score 16.8; DB 9; Length 71;
Best Local Similarity 60.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 8 UUGAGCCUCAGGUCUGAGU 27
+|||||:|:|:|:|:|:|
Db 50 TTGAGACTCTGCGTCTGAGT 69

Search completed: December 21, 2002, 12:57:43
Job time : 387.596 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 372.278 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-27
Perfect score: 26
Sequence: 1 CACTCAGCCACTGATTAAACAGAG 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_ov:*
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6: gb_ov:*
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41: gb_ov:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	26	100.0	52 6 A93226	A93226 Sequence 49
C 2	26	100.0	53 6 A93224	A93224 Sequence 47
C 3	26	100.0	54 6 A93225	A93225 Sequence 48
C 4	26	100.0	55 6 A93227	A93227 Sequence 50
C 5	26	100.0	56 6 A93228	A93228 Sequence 51
C 6	26	100.0	56 6 I12446	I12446 Sequence 16
C 7	26	100.0	56 6 I14508	I14508 Sequence 16
C 8	26	100.0	57 6 A93229	A93229 Sequence 52
C 9	26	100.0	58 6 A93230	A93230 Sequence 53
C 10	26	100.0	59 6 A93231	A93231 Sequence 54
C 11	26	100.0	90 6 HUMPCRAL	M25947 Human chron
C 12	26	100.0	40 6 A93231	AR153123 Sequence
C 13	25	96.2	41 6 A93232	AR153124 Sequence
C 14	25	96.2	58 6 BD001711	BD001711 Composi
C 15	25	96.2	58 6 BD001724	BD001724 Method
C 16	25	96.2	59 6 BD001724	BD001724 Composi
C 17	25	96.2	59 6 BD001723	BD001723 Method
C 18	25	96.2	60 6 A50294	A50294 Sequence 14
C 19	25	96.2	66 6 I14505	I14505 Sequence 13
C 20	25	96.2	66 6 A93231	AR037937 Sequence
C 21	21.4	82.3	40 6 AR037937	AR037937 Sequence
C 22	21	80.8	44 6 AX280264	AX280264 Sequence
C 23	20	76.9	44 6 AX280265	AX280265 Sequence
C 24	20	76.9	47 6 AX280256	AX280256 Sequence
C 25	20	76.9	47 6 AX280259	AX280259 Sequence
C 26	19.4	74.6	41 6 AX280254	AX280254 Sequence
C 27	19	73.1	41 6 AX280255	AX280255 Sequence
C 28	19	73.1	41 6 AR037938	AR037938 Sequence
C 29	18	69.2	18 6 NM0240055	AJ240055 Mus muscu
C 30	17.2	66.2	68 10 R0240056	AJ240056 Rattus no
C 31	17.2	66.2	68 10 R0240056	AJ240056 Rattus no
C 32	16.4	63.1	31 6 AK243934	BD000491 Process f
C 33	16.4	63.1	31 6 AK243934	BD000491 Process f
C 34	16	61.5	30 6 AX199556	AX199556 Sequence
C 35	16	61.5	50 6 AX199556	AX199556 Sequence
C 36	16	61.5	50 6 AX199558	AX199558 Sequence
C 37	16	61.5	51 6 A38299	A38299 Sequence 33
C 38	16	61.5	88 6 AR193111	AR193111 Sequence
C 39	15.8	60.8	21 6 AX092761	AX092761 Sequence
C 40	15.8	60.8	21 6 AX059982	AX059982 Sequence
C 41	15	57.7	41 6 AR153125	AR153125 Sequence
C 42	15	57.7	22 6 AR153126	AR153126 Sequence
C 43	15	57.7	22 6 AR153126	AR153126 Sequence
C 44	15	57.7	22 6 AR163303	AR163303 Sequence
C 45	14.8	56.9	18 6 AR163304	AR163304 Sequence
C 45	14.8	56.9	18 6 AR037940	AR037940 Sequence

ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	52 bp	DNA	linear	PAT 22-JAN-2000
A93226/c	A93226	Sequence 49 from Patent WO9746672.				
ACCESION	A93226					
VERSION	A93226.1	GI:6741611				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						

FEATURES
source
Location/Qualifiers
1..52
/db_xref="taxon:32644"
BASE COUNT 12 a 10 c 16 g 14 t
ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAACAGAG 26
Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 2
LOCUS A93224/c 53 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 47 from Patent WO9746672.
ACCESSION A93224
VERSION A93224.1 GI:6741609
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 53)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 47 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES
source
Location/Qualifiers
1..53
/db_xref="taxon:32644"

BASE COUNT 13 a 10 c 16 g 14 t
ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAACAGAG 26
Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 3
LOCUS A93225/c 54 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 48 from Patent WO9746672.
ACCESSION A93225
VERSION A93225.1 GI:6741610
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 54)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 48 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES
source
Location/Qualifiers
1..54
/db_xref="taxon:32644"

BASE COUNT 13 a 10 c 16 g 15 t
ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAACAGAG 26
Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 4
LOCUS A93227/c 55 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 50 from Patent WO9746672.
ACCESSION A93227
VERSION A93227.1 GI:6741612
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 55)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 50 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES
source
Location/Qualifiers
1..55
/db_xref="taxon:32644"

BASE COUNT 13 a 10 c 16 g 16 t
ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAACAGAG 26
Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 5
LOCUS A93228 56 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 51 from Patent WO9746672.
ACCESSION A93228
VERSION A93228.1 GI:6741613
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 56)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 51 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES
source
Location/Qualifiers
1..56
/db_xref="taxon:32644"

BASE COUNT 13 a 11 c 16 g 16 t
ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAACAGAG 26
Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 6
LOCUS I12446 56 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 16 from patent US 5424413.
ACCESSION I12446
VERSION I12446.1 GI:909830

KEYWORDS
SOURCE unknown.
ORGANISM unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 56)
TITLE Hogan, J.J., Arnold, L.J. Jr., Nelson, N.C. and Bezerkov, R.
JOURNAL Branched nucleic acid probes
Patent: US 5424413-A 16 13-JUN-1995;
FEATURES Location/Qualifiers
source 1..56

BASE COUNT 16 a 17 c 9 g 14 t

ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTCAGCCACTGATTTAAGCAG 26
Db 10 CACTCAGCCACTGATTTAAGCAG 35

RESULT 7
LOCUS 114508 56 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 16 from patent US 5451503.
ACCESSION 114508
VERSION 114508.1 GI:996991
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 56)
TITLE Hogan, J.J., Arnold, L.J. Jr., Nelson, N.C. and Bezerkov, R.
JOURNAL Patent: US 5451503-A 16 19-SEP-1995;
FEATURES Location/Qualifiers
source 1..56

BASE COUNT 16 a 17 c 9 g 14 t

ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTCAGCCACTGATTTAAGCAG 26
Db 10 CACTCAGCCACTGATTTAAGCAG 35

RESULT 8
LOCUS A93229 57 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 52 from Patent WO9746672.
ACCESSION A93229
VERSION A93229.1 GI:6741614
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 57)
TITLE Sczakiel, G. and Haas, R.
JOURNAL ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
Patent: WO 9746672-A 52 11-DEC-1997;
FEATURES Location/Qualifiers
source 1..57

BASE COUNT 14 a 11 c 16 g 16 t

ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTCAGCCACTGATTTAAGCAG 26
Db 43 CACTCAGCCACTGATTTAAGCAG 18

RESULT 9
LOCUS A93230 58 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 53 from Patent WO9746672.
ACCESSION A93230
VERSION A93230.1 GI:6741615
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 58)
TITLE Sczakiel, G. and Haas, R.
JOURNAL ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
Patent: WO 9746672-A 53 11-DEC-1997;
FEATURES Location/Qualifiers
source 1..58

BASE COUNT 14 a 11 c 17 g 16 t

ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTCAGCCACTGATTTAAGCAG 26
Db 43 CACTCAGCCACTGATTTAAGCAG 18

RESULT 10
LOCUS A93231 59 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 54 from Patent WO9746672.
ACCESSION A93231
VERSION A93231.1 GI:6741616
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 59)
TITLE Sczakiel, G. and Haas, R.
JOURNAL ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
Patent: WO 9746672-A 54 11-DEC-1997;
FEATURES Location/Qualifiers
source 1..59

BASE COUNT 15 a 11 c 17 g 16 t

ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTCAGCCACTGATTTAAGCAG 26
Db 43 CACTCAGCCACTGATTTAAGCAG 18

RESULT 11

HOMBCRA1
 LOCUS HOMBCRA1 90 bp DNA linear PRI 27-APR-1993
 DEFINITION Human chronic myelocytic leukemia c-abl oncogene breakpoint cluster
 region (bcr) DNA, exon b3.
 ACCESSION M25947
 VERSION M25947.1 GI:1179381
 KEYWORDS breakpoint cluster region; c-abl oncogene; chronic myelocytic leukemia.
 SEGMENT 1 of 3
 SOURCE Human fibroblast cell line K562, cDNA to mRNA, clone pV1-3.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 90)
 AUTHORS De Klein,A., Hermans,A., Bootsma,D., Grosveld,G., Heisterkamp,N., Stam,K. and Groffen,J.
 TITLE The role of the Philadelphia translocation in chronic myelocytic leukemia
 JOURNAL Ann. Clin. Res. 18 (5-6), 278-283 (1986)
 MEDLINE 87183193
 PUBMED 3471171
 FEATURES
 SOURCE Location/Qualifiers
 1..90
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 /db_xref="taxon:9606"
 exon <1..75
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 BASE COUNT 20 a 18 c 24 g 28 t
 ORIGIN
 Query Match 100.0%; Score 26; DB 9; Length 90;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CACTCAGCCACTGGATTAAACGAG 26
 Db 45 CACTCAGCCACTGGATTAAACGAG 70
 RESULT 12
 ARI53123/C ARI53123 40 bp DNA linear PAT 08-AUG-2001
 LOCUS ARI53123
 DEFINITION Sequence 125 from patent US 6235480.
 ACCESSION ARI53123
 VERSION ARI53123.1 GI:15120655
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D., Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T., Olson,R.J., Wood,K.V. and Welch,R.
 TITLE Detection of nucleic acid hybrids
 JOURNAL Patent: US 6235480-A 125 22-MAY-2001;
 FEATURES
 source Location/Qualifiers
 1..40
 /organism="unknown"
 BASE COUNT 10 a 9 c 8 g 13 t
 ORIGIN
 Query Match 96.2%; Score 25; DB 6; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ACTCAGCCACTGGATTAAACGAG 26
 Db 40 ACTCAGCCACTGGATTAAACGAG 16
 RESULT 13
 ARI53124/C ARI53124 41 bp DNA linear PAT 08-AUG-2001
 LOCUS

DEFINITION Sequence 126 from patent US 6235480.
 ACCESSION ARI53124
 VERSION ARI53124.1 GI:15120656
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 41)
 AUTHORS Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D., Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T., Olson,R.J., Wood,K.V. and Welch,R.
 TITLE Detection of nucleic acid hybrids
 JOURNAL Patent: US 6235480-A 126 22-MAY-2001;
 FEATURES
 source Location/Qualifiers
 1..41
 /organism="unknown"
 BASE COUNT 9 a 8 c 11 g 13 t
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 Query Match 96.2%; Score 25; DB 6; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ACTCAGCCACTGGATTAAACGAG 26
 Db 41 ACTCAGCCACTGGATTAAACGAG 17
 RESULT 14
 BD001711 BD001711 58 bp DNA linear PAT 31-JAN-2002
 LOCUS BD001711
 DEFINITION Compositions for homogeneous protection assay.
 ACCESSION BD001711
 VERSION BD001711.1 GI:18626270
 KEYWORDS JP 2000350598-A/13.
 SOURCE JP 2000350598-A/13.
 ORGANISM
 REFERENCE 1 (bases 1 to 58)
 AUTHORS J.R.A. and Nelson,N.C.
 TITLE Compositions for homogeneous protection assay
 JOURNAL Patent: JP 2000350598-A 13 19-DEC-2000;
 COMMENT GEN PROBE INC
 OS Artificial Sequence
 PN JP 2000350598-A/13
 PD 19-DEC-2000
 PE 02-MAY-2000 JP 2000133493
 PR 21-SEP-1987 US 099.392
 PI RYLE JOHN ARNOLD JR,NORMAN C NELSON
 PC C12Q1/68,C12N15/09,C12Q1/66,G01N31/78,G01N33/53,G01N33/58, PC
 C12N15/00
 CC
 FH Key
 FT source Location/Qualifiers
 1..58
 /organism="Artificial Sequence".
 FEATURES
 source Location/Qualifiers
 1..58
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 BASE COUNT 14 a 15 c 13 g 16 t
 ORIGIN
 Query Match 96.2%; Score 25; DB 6; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ACTCAGCCACTGGATTAAACGAG 26
 Db 1 ACTCAGCCACTGGATTAAACGAG 25
 RESULT 15
 BD001724

1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 : Search time 257.731 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-26

Perfect score: 18

Sequence: 1 GCAATCATCGAGCATG 18

Scoring table: IDENTITY_NDC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank

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2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

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9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pin:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hcg_hum:*

40: em_hcg_mus:*

41: em_hcg_other:*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	14.8	82.2	99	3	TTSNRNA	X65863 T.thermophil
2	13.8	76.7	37	6	158617	158617 Sequence 3
3	13.8	76.7	37	6	163515	163515 Sequence 3
4	13.8	76.7	73	6	AR174784	AR174784 Sequence
5	13.4	74.4	50	6	AX162242	AX162242 Sequence
6	13.2	73.3	54	5	CHKIGHAD	M30369 Gallus gall
7	13.2	73.3	55	5	CHKIGHAD	M30354 Gallus gall
8	13.2	73.3	57	5	CHKIGHAD	M30351 Gallus gall
9	13.2	73.3	63	5	CHKIGHAD	M30353 Gallus gall
10	13.2	73.3	66	5	CHKIGHAD	M30357 Gallus gall
11	13.2	73.3	69	5	CHKIGHAD	M30356 Gallus gall
12	13.2	73.3	69	5	CHKIGHAD	M30358 Gallus gall
13	13.2	73.3	69	5	CHKIGHAD	M30356 Gallus gall
14	13.2	73.3	69	5	CHKIGHAD	M30356 Gallus gall
15	13.2	73.3	69	5	CHKIGHAD	M30356 Gallus gall
16	13.2	73.3	72	5	CHKIGHAD	M30355 Gallus gall
17	13.2	73.3	72	5	CHKIGHAD	M30357 Gallus gall
18	13.2	73.3	75	5	CHKIGHAD	M30357 Gallus gall
19	12.8	71.1	20	6	AR008075	AR008075 Sequence
20	12.8	71.1	20	6	AR031291	AR031291 Sequence
21	12.8	71.1	20	6	AR087476	AR087476 Sequence
22	12.8	71.1	20	6	AR102189	AR102189 Sequence
23	12.8	71.1	20	6	AR102200	AR102200 Sequence
24	12.8	71.1	20	6	AR110665	AR110665 Sequence
25	12.8	71.1	20	6	AR137590	AR137590 Sequence
26	12.8	71.1	20	6	AR154582	AR154582 Sequence
27	12.8	71.1	20	6	AR179852	AR179852 Sequence
28	12.8	71.1	20	6	164537	164537 Sequence 13
29	12.8	71.1	23	6	AR008076	AR008076 Sequence
30	12.8	71.1	23	6	AR031292	AR031292 Sequence
31	12.8	71.1	23	6	AR087477	AR087477 Sequence
32	12.8	71.1	23	6	AR102190	AR102190 Sequence
33	12.8	71.1	23	6	AR102201	AR102201 Sequence
34	12.8	71.1	23	6	AR110666	AR110666 Sequence
35	12.8	71.1	23	6	AR137591	AR137591 Sequence
36	12.8	71.1	23	6	AR154583	AR154583 Sequence
37	12.8	71.1	23	6	AR179853	AR179853 Sequence
38	12.8	71.1	23	6	164538	164538 Sequence 14
39	12.4	68.9	21	6	AX296863	AX296863 Sequence
40	12.4	68.9	21	6	AR1364	AR1364 Sequence 9
41	12.4	68.9	24	6	AX001584	AX001584 Sequence
C 42	12.4	68.9	24	6	AX292230	AX292230 Sequence
C 43	12.2	67.8	23	6	AX317694	AX317694 Sequence
C 44	12.2	67.8	23	6	AX402944	AX402944 Sequence
C 45	12.2	67.8	24	6	AR210302	AR210302 Sequence

ALIGNMENTS

RESULT 1

LOCUS TTSNRNA

DEFINITION T.thermophila snRNA.

ACCESSION X65863

VERSION X65863.1 GI:10842

KEYWORDS small nuclear RNA.

SOURCE Tetrahymena thermophila.

ORGANISM Tetrahymena thermophila.

REFERENCE Eukaryota, Alveolata; Ciliophora; Oligohymenophorea;

AUTHORS Hymenostomatida; Tetrahymena; Tetrahymena.

TITLE I (bases 1 to 99)

JOURNAL Engberg, J.

Submitted (27-APR-1992) J. Engberg, The Royal Danish School of

Pharmacy, Dept of Biological Sciences, 2 Universitetsparken, 2100
Copenhagen, DENMARK

REFERENCE 2 (bases 1 to 99)
AUTHORS Orum, H., Nielsen, H. and Engberg, J.
TITLE Sequence of a new snRNA from the ciliate *Tetrahymena thermophila*
JOURNAL Nucleic Acids Res. 20 (13), 3518 (1992)
MEDLINE 9235014
PUBMED 1630929

FEATURES
source Location/Qualifiers
1..99
/organism="Tetrahymena thermophila"
/strain="B186VIT"
/db_xref="taxon:5911"

snRNA 32 a 22 c 19 g 25 t 1 others
BASE COUNT
ORIGIN

Query Match 82.2%; Score 14.8; DB 3; Length 99;
Best Local Similarity 88.9%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 18
Db 82 GGAATCATCGAGCATG 65

RESULT 2
LOCUS 158617 158617 37 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5652210.
ACCESSION 158617
VERSION 158617.1 GI:2477855
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 37)
AUTHORS Barr, P.J., Shapiro, J.P. and Kiefer, M.C.
TITLE Soluble splice variant of the Fas (Apo-1) antigen, Fas, DELTA, TM
JOURNAL Patent: US 5652210-A 3 29-JUL-1997;
FEATURES Location/Qualifiers
source 1..37
/organism="unknown"

BASE COUNT 12 a 8 c 8 g 9 t
ORIGIN

Query Match 76.7%; Score 13.8; DB 6; Length 37;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
Db 14 GGAATCATCAAGCATG 30

RESULT 3
LOCUS 163515 163515 37 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5663070.
ACCESSION 163515
VERSION 163515.1 GI:2481088
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 37)
AUTHORS Barr, P.J., Shapiro, J.P. and Kiefer, M.C.
TITLE Recombinant production of a soluble splice variant of the Fas (Apo-1) antigen, fas TM
JOURNAL Patent: US 5663070-A 3 02-SEP-1997;
FEATURES Location/Qualifiers
source 1..37
/organism="unknown"

BASE COUNT 12 a 8 c 8 g 9 t
ORIGIN

Query Match 76.7%; Score 13.8; DB 6; Length 37;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
Db 14 GGAATCATCAAGCATG 30

RESULT 4
LOCUS AR174784 AR174784 73 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 36 from patent US 6307037.
ACCESSION AR174784
VERSION AR174784.1 GI:17915104
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gaffney, T. Deane, J., Flavler, A., Cloyd Kirksey, M.M., Philippsen, P., Dietrich, F., Wendland, J., Bernasconi, P., White, K. and Filipowicz, W.
TITLE Fungal target genes and methods
JOURNAL Patent: US 6307037-A 36 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..73
/organism="unknown"

BASE COUNT 23 a 16 c 17 g 17 t
ORIGIN

Query Match 76.7%; Score 13.8; DB 6; Length 73;
Best Local Similarity 88.2%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
Db 44 GGAATCATCGAGCATG 60

RESULT 5
LOCUS AX162242 AX162242 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5570 from Patent WO0140521.
ACCESSION AX162242
VERSION AX162242.1 GI:14543573
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5570 07-JUN-2001;
FEATURES Curagen Corporation (US)
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc.feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number c94400660"

misc.feature

BASE COUNT 13 a 14 c 13 g 10 t
ORIGIN

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Best Local Similarity 93.3%; Pred. No. 1.8e+04;

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATCATCGAGCGATGG 18
    |||||||||
Db 17 ATCATCGAGCGATGG 31

RESULT 6
CHRGVHABD 54 bp mRNA linear VRT 12-OCT-1994
LOCUS Gallus gallus (clone 3W-101) Ig rearranged heavy chain D region
DEFINITION mRNA, partial cds.
ACCESSION M30369
VERSION M30369.1 GI:557505
KEYWORDS Ig heavy chain; Igm; diversity region; immunoglobulin;
SOURCE immunoglobulin heavy chain; mu-immunoglobulin; processed gene;
Gallus gallus (strain CB inbred line) 21 day old neonate cDNA to
mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 54)
AUTHORS Reynaud,C.A., Dahan,A., Anguez,V. and Weill,J.C.
TITLE Somatic hyperconversion diversifies the single Vh gene of the
JOURNAL chicken with a high incidence in the D region
MEDLINE Cell 59 (1), 171-183 (1989)
PUBMED 90003227
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QY 1 GGATTCATCGAGCGATGG 18
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Db 37 GGTAGCATCGAGCGATGG 54

RESULT 7
CHRGVHABD 55 bp mRNA linear VRT 12-OCT-1994
LOCUS Gallus gallus (clone 18D-5) Ig rearranged heavy chain D region
DEFINITION mRNA, partial.
ACCESSION M30354
VERSION M30354.1 GI:557529
KEYWORDS Ig heavy chain; Ig variable region; Igm; diversity region;
immunoglobulin; immunoglobulin heavy chain; mu-immunoglobulin;
processed gene; rearranged.
SOURCE Gallus gallus (strain CB inbred line) 18 day old embryo cDNA to
mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 55)
AUTHORS Reynaud,C.A., Dahan,A., Anguez,V. and Weill,J.C.
TITLE Somatic hyperconversion diversifies the single Vh gene of the
JOURNAL chicken with a high incidence in the D region
MEDLINE Cell 59 (1), 171-183 (1989)
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGATTCATCGAGCGATGG 18
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Db 40 GGTAGCATCGAGCGATGG 57

RESULT 9
CHRGVHABD 63 bp mRNA linear VRT 12-OCT-1994
LOCUS Gallus gallus (clone 18D-2) Ig rearranged heavy chain D region
DEFINITION mRNA, partial.
ACCESSION M30352
VERSION M30352.1 GI:557527
KEYWORDS Ig heavy chain; Ig variable region; Igm; diversity region;

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SOURCE immunoglobulin; immunoglobulin heavy chain; mu-immunoglobulin; processed gene; rearranged.
Gallus gallus (strain CB inbred line) 18 day old embryo cDNA to mRNA.

ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 63)
Keynaud, C.A., Dahan, A., Anguez, V. and Weill, J.C.
Somatic hyperconversion diversifies the single Vh gene of the chicken with a high incidence in the D region

JOURNAL Cell 59 (1), 171-183 (1989)

MEDLINE 90003227

PUBMED 2507167

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 46 GTTAGCATCGAGCATCG 63

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LOCUS
DEFINITION
Gallus gallus (clone 3W-31) Ig rearranged heavy chain D region
M30367
VERSION
M30367.1 GI:557503
KEYWORDS
Ig heavy chain; IGM; diversity region; immunoglobulin; immunoglobulin heavy chain; mu-immunoglobulin; processed gene.
SOURCE
Gallus gallus (strain CB inbred line) 21 day old neonate cDNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 66)
Keynaud, C.A., Dahan, A., Anguez, V. and Weill, J.C.
Somatic hyperconversion diversifies the single Vh gene of the chicken with a high incidence in the D region

JOURNAL Cell 59 (1), 171-183 (1989)

MEDLINE 90003227

PUBMED 2507167

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAATCATCGAGCATCG 18
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Db 49 GTTAGCATCGAGCATCG 66

RESULT 11
CHKIGHAAN
LOCUS
DEFINITION
Gallus gallus (clone 18D-4) Ig rearranged heavy chain D region
M30353
VERSION
M30353.1 GI:557528
KEYWORDS
Ig heavy chain; Ig variable region; IGM; diversity region; immunoglobulin; immunoglobulin heavy chain; mu-immunoglobulin; processed gene; rearranged.
SOURCE
Gallus gallus (strain CB inbred line) 18 day old embryo cDNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 69)
Keynaud, C.A., Dahan, A., Anguez, V. and Weill, J.C.
Somatic hyperconversion diversifies the single Vh gene of the chicken with a high incidence in the D region

JOURNAL Cell 59 (1), 171-183 (1989)

MEDLINE 90003227

PUBMED 2507167

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 52 GTTAGCATCGAGCATCG 69

RESULT 12
CHKIGHAAB
LOCUS
DEFINITION
Gallus gallus (clone 18D-9) Ig rearranged heavy chain D region
M30356
VERSION
M30356.1 GI:557531
KEYWORDS
Ig heavy chain; Ig variable region; IGM; diversity region; immunoglobulin; immunoglobulin heavy chain; mu-immunoglobulin; processed gene; rearranged.
SOURCE
Gallus gallus (strain CB inbred line) 18 day old embryo cDNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 69)
Keynaud, C.A., Dahan, A., Anguez, V. and Weill, J.C.
Somatic hyperconversion diversifies the single Vh gene of the chicken with a high incidence in the D region

JOURNAL Cell 59 (1), 171-183 (1989)

MEDLINE 90003227

PUBMED 2507167

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Db      52 GGTACATCGACGCATGG 69

RESULT 13
CHRGHAB
LOCUS      Gallus gallus (clone 3W-1) Ig Rearranged heavy chain D region mRNA,
DEFINITION      partial cds.
ACCESSION      M30358.1 GI:557494
VERSION      M30358.1 GI:557494
KEYWORDS      Ig heavy chain; Igm; diversity region; immunoglobulin;
SOURCE      immunoglobulin heavy chain; mu-immunoglobulin; processed gene.
ORGANISM      Gallus gallus (strain CB Inbred line) 21 day old neonate cDNA to
      mRNA.
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Archosaustra; Aves; Neognathae; Galliformes; Phasianidae;
      Phasianinae; Gallus.
      1 (bases 1 to 69)
REFERENCE      Reynaud,C.A., Dahan,A., Anguez,V. and Weill,J.C.
      Somatic hyperconversion diversifies the single Vh gene of the
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JOURNAL      90003227
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  Best Local Similarity 83.3%; Pred. No. 2.3e+04;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAATCATCGAGCGCATGG 18
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Db      52 GGTACATCGACGCATGG 69

RESULT 14
CHRGHAB
LOCUS      Gallus gallus (clone 3W-21) Ig Rearranged heavy chain D region
DEFINITION      mRNA, partial cds.
ACCESSION      M30364.1 GI:557500
VERSION      M30364.1 GI:557500
KEYWORDS      Ig heavy chain; Igm; diversity region; immunoglobulin;
SOURCE      immunoglobulin heavy chain; mu-immunoglobulin; processed gene.
ORGANISM      Gallus gallus (strain CB Inbred line) 21 day old neonate cDNA to
      mRNA.
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Archosaustra; Aves; Neognathae; Galliformes; Phasianidae;
      Phasianinae; Gallus.
      1 (bases 1 to 69)
REFERENCE      Reynaud,C.A., Dahan,A., Anguez,V. and Weill,J.C.
      Somatic hyperconversion diversifies the single Vh gene of the
      chicken with a high incidence in the D region
      Cell 59 (1), 171-183 (1989)
JOURNAL      90003227
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  Best Local Similarity 83.3%; Pred. No. 2.3e+04;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAATCATCGAGCGCATGG 18
      ||| ||||| |||||
Db      52 GGTACATCGACGCATGG 69

RESULT 15
CHRGHAB
LOCUS      Gallus gallus (clone 3W-93) Ig Rearranged heavy chain D region
DEFINITION      mRNA, partial cds.
ACCESSION      M30368.1 GI:557504
VERSION      M30368.1 GI:557504
KEYWORDS      Ig heavy chain; Igm; diversity region; immunoglobulin;
SOURCE      immunoglobulin heavy chain; mu-immunoglobulin; processed gene.
ORGANISM      Gallus gallus (strain CB Inbred line) 21 day old neonate cDNA to
      mRNA.
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Archosaustra; Aves; Neognathae; Galliformes; Phasianidae;
      Phasianinae; Gallus.
      1 (bases 1 to 69)
REFERENCE      Reynaud,C.A., Dahan,A., Anguez,V. and Weill,J.C.
      Somatic hyperconversion diversifies the single Vh gene of the
      chicken with a high incidence in the D region
      Cell 59 (1), 171-183 (1989)
JOURNAL      90003227
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  Best Local Similarity 83.3%; Pred. No. 2.3e+04;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGAATCATCGAGCGCATGG 18
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Db      52 GGTACATCGACGCATGG 69
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Db 52 GGTAGCATCGACCATGG 69

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Job time : 261.731 secs

Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 ; Search time 38.1306 Seconds
(without alignments)
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Title: US-09-121-239-1
Perfect score: 54
Sequence: 1 TAAATTAATAGACTGACTACTA.....CCCTGAGCTCAAGTCAGA 54

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 35696 seqs, 198428768 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	55.6	55	10	US-09-944-036-45 Sequence 45, Appl
3	29.6	54.8	53	10	US-09-202-972-11 Sequence 11, Appl
4	29.4	54.4	49	10	US-09-875-408-1 Sequence 1, Appl
5	29.4	54.4	49	12	US-10-075-579-1 Sequence 1, Appl
6	28.2	52.2	53	12	US-09-875-408-13 Sequence 13, Appl
7	28.2	52.2	53	10	US-10-075-579-13 Sequence 13, Appl
8	28	51.9	30	10	US-09-876-527-29 Sequence 29, Appl
9	28	51.9	33	9	US-10-001-407-29 Sequence 29, Appl
10	28	51.9	33	10	US-09-738-972-10 Sequence 10, Appl
11	28	51.9	33	10	US-09-944-036-4 Sequence 4, Appl
12	28	51.9	35	10	US-09-202-972-15 Sequence 15, Appl
13	28	51.9	35	10	US-09-202-972-17 Sequence 17, Appl
14	28	51.9	37	10	US-09-944-036-2 Sequence 2, Appl
15	28	51.9	41	10	US-09-953-321-15 Sequence 15, Appl
16	28	51.9	51	10	US-09-944-036-41 Sequence 41, Appl
17	28	51.9	52	10	US-09-944-036-39 Sequence 39, Appl
18	28	51.9	52	10	US-09-944-036-43 Sequence 43, Appl
19	28	51.9	53	10	US-09-944-036-34 Sequence 34, Appl

20	28	51.9	53	10	US-09-944-036-35 Sequence 35, Appl
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22	28	51.9	53	10	US-09-944-036-37 Sequence 37, Appl
23	28	51.9	53	10	US-09-944-036-38 Sequence 38, Appl
24	28	51.9	53	10	US-09-944-036-42 Sequence 42, Appl
25	28	51.9	54	10	US-09-944-036-6 Sequence 6, Appl
26	28	51.9	54	10	US-09-944-036-9 Sequence 9, Appl
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33	28	51.9	58	9	US-10-001-407-19 Sequence 19, Appl
34	28	51.9	59	10	US-09-738-972-11 Sequence 11, Appl
35	28	51.9	59	10	US-09-738-972-2 Sequence 2, Appl
36	28	51.9	61	10	US-09-738-972-12 Sequence 12, Appl
37	28	51.9	61	10	US-09-983-321-5 Sequence 5, Appl
38	28	51.9	63	10	US-09-983-321-5 Sequence 5, Appl
39	27.6	51.1	51	10	US-09-866-778A-34 Sequence 34, Appl
40	27.4	50.7	51	10	US-09-975-408-56 Sequence 56, Appl
41	27.2	50.4	47	10	US-10-075-579-56 Sequence 56, Appl
42	27.2	50.4	47	12	US-09-202-972-18 Sequence 18, Appl
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ALIGNMENTS

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US-09-944-036-40
Sequence 40, Application US/0944036
Patient No. US2002005035A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERRET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.0T
CURRENT APPLICATION NUMBER: US/09/944,036
PRIORITY FILING DATE: 2001-08-31
PRIORITY FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 51
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
NAME/KEY: promoter
LOCATION: (1)..(29)
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Best Local Similarity 76.5%; Pred. No. 0.00064;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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DB 1 AATTAATAGACTGACTACTATAGGAGACTGAGACCTCAAGTCGA 51
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US-09-944-036-45

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; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: APPLICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: G9114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
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; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
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RESULT 3
US-09-202-972-11
; Sequence 11, Application US/09202972
; Patent No. US20020025518A1
; GENERAL INFORMATION:
; APPLICANT: Hirose, Minoru
; APPLICANT: Hashimoto, Junko
; APPLICANT: Yoshimura, Tadashi
; TITLE OF INVENTION: METHOD FOR THE DETECTION OF TELOMERASE ACTIVITY
; FILE REFERENCE: sequence listing for 382,1024
; CURRENT APPLICATION NUMBER: US/09/202,972
; EARLIER FILING DATE: 1998-12-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02251
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-202-972-11
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Best Local Similarity 79.5%; Pred. No. 0.0049;
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RESULT 4
US-09-975-408-1
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; Sequence 1, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 267/174 Patrick S. Bagleman
; CURRENT APPLICATION NUMBER: US/09/975,408
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-09-975-408-1
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OY 6 TAATACGACTCCTACTATAGGAGACTGACACCCCTGAGGCT 44
Db 1 TAATACGACTCCTACTATAGGAGAGACAGACAACTGAGTGT 39
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RESULT 5
US-10-075-579-1
; Sequence 1, Application US/10075579
; Patent No. US20020119484A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 256/262 Patrick S. Bagleman
; CURRENT APPLICATION NUMBER: US/10/075,579
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-10-075-579-1
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Query Match          54.4%; Score 29.4; DB 12; Length 49;
Best Local Similarity 84.6%; Pred. No. 0.0058;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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OY 6 TAATACGACTCCTACTATAGGAGACTGACACCCCTGAGGCT 44
Db 1 TAATACGACTCCTACTATAGGAGAGACAGAACTGAGTGT 39
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RESULT 6
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US-09-975-408-13
; Sequence 13, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
; FILE REFERENCE: 267/174 Patrick S. Eagelman
; CURRENT APPLICATION NUMBER: US/09/975,408
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-975-408-13

Query Match      52.2%; Score 28.2; DB 10; Length 53;
Best Local Similarity 80.5%; Pred. No. 0.018; 8; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 8;

QY 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42
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DB 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42

RESULT 7
US-10-075-579-13
; Sequence 13, Application US/10075579
; Patent No. US20020119484A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
; FILE REFERENCE: 256/263 Patrick S. Eagelman
; CURRENT APPLICATION NUMBER: US/10/075,579
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/710,200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-075-579-13

Query Match      52.2%; Score 28.2; DB 12; Length 53;
Best Local Similarity 80.5%; Pred. No. 0.018; 8; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 8;

QY 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42
    |||||||||||||||||||||||||||
DB 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42

RESULT 8
US-09-876-527-29
; Sequence 29, Application US/09876527
; Patent No. US20020102616A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Jelinek, Laura J.
; APPLICANT: Sheppard, Paul O.
```

```

; Hagopian, William A.
; Lagasse, James M.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,527
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,481
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ringenfelder, Susan
; REGISTRATION NUMBER: P-41,156
; REFERENCE/DOCKET NUMBER: 95-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC11197
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-876-527-29

Query Match      51.9%; Score 28; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.018; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

QY 2 AAATTATAGACTCTACTATAGGAGAG 29
    |||||||||||||||||||||||
DB 1 AAATTATAGACTCTACTATAGGAGAG 28

RESULT 9
US-10-001-407-29
; Sequence 29, Application US/10001407
; Patent No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Butrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP17-03-07
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 29
; LENGTH: 33
; TYPE: DNA
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ORGANISM: HIV-2
US-10-001-407-29

Query Match
Best Local Similarity 100.0%; Score 28; DB 9; Length 33;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29
|||||
DB 2 AATTAATACGACTCATTATAGGAGAC 29

RESULT 10

US-09-738-972-10
Sequence 10, Application US/09738972
Patent No. US20020012918A1
GENERAL INFORMATION:
APPLICANT: BRENTANO, Steven T.
APPLICANT: LANKFORD, Roger L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
FILE REFERENCE: GP19-02.UT
CURRENT APPLICATION NUMBER: US/09/738,972
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/171,202
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: promoter
US-09-738-972-10

Query Match
Best Local Similarity 100.0%; Score 28; DB 10; Length 33;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29
|||||
DB 2 AATTAATACGACTCATTATAGGAGAC 29

RESULT 11

US-09-944-036-4
Sequence 4, Application US/09944036
Patent No. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasun Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 17 promoter
NAME/KEY: promoter
LOCATION: (1)..(33)

US-09-944-036-4

Query Match
Best Local Similarity 100.0%; Score 28; DB 10; Length 33;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29
|||||
DB 2 AATTAATACGACTCATTATAGGAGAC 29

RESULT 12

US-09-202-972-15
Sequence 15, Application US/09202972
Patent No. US20020025518A1
GENERAL INFORMATION:
APPLICANT: Hirose, Junko
APPLICANT: Yoshimura, Tadashi
TITLE OF INVENTION: METHOD FOR THE DETECTION OF TELOMERASE ACTIVITY
FILE REFERENCE: sequence listing for 382.1024
CURRENT APPLICATION NUMBER: US/09/202,972
CURRENT FILING DATE: 1998-12-23
EARLIER APPLICATION NUMBER: PCT/JP97/02251
EARLIER FILING DATE: 1997-06-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-202-972-15

Query Match
Best Local Similarity 100.0%; Score 28; DB 10; Length 35;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTATACGACTCATTATAGGAGAC 28
|||||
DB 6 TAAATTATACGACTCATTATAGGAGAC 33

RESULT 13

US-09-202-972-17
Sequence 17, Application US/09202972
Patent No. US20020025518A1
GENERAL INFORMATION:
APPLICANT: Hirose, Junko
APPLICANT: Yoshimura, Tadashi
TITLE OF INVENTION: METHOD FOR THE DETECTION OF TELOMERASE ACTIVITY
FILE REFERENCE: sequence listing for 382.1024
CURRENT APPLICATION NUMBER: US/09/202,972
CURRENT FILING DATE: 1998-12-23
EARLIER APPLICATION NUMBER: PCT/JP97/02251
EARLIER FILING DATE: 1997-06-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-202-972-17

Query Match
Best Local Similarity 100.0%; Score 28; DB 10; Length 35;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29

DB 7 AAATTAATACGACTCCTACTATAGGAGAC 34

RESULT 14
US-09-944-036-2

Sequence 2, Application US/09944036
Patent No. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP14-02.UF
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
NAME/KEY: Promoter
LOCATION: (1)...(29)
US-09-944-036-2

Query Match 51.9%; Score 28; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

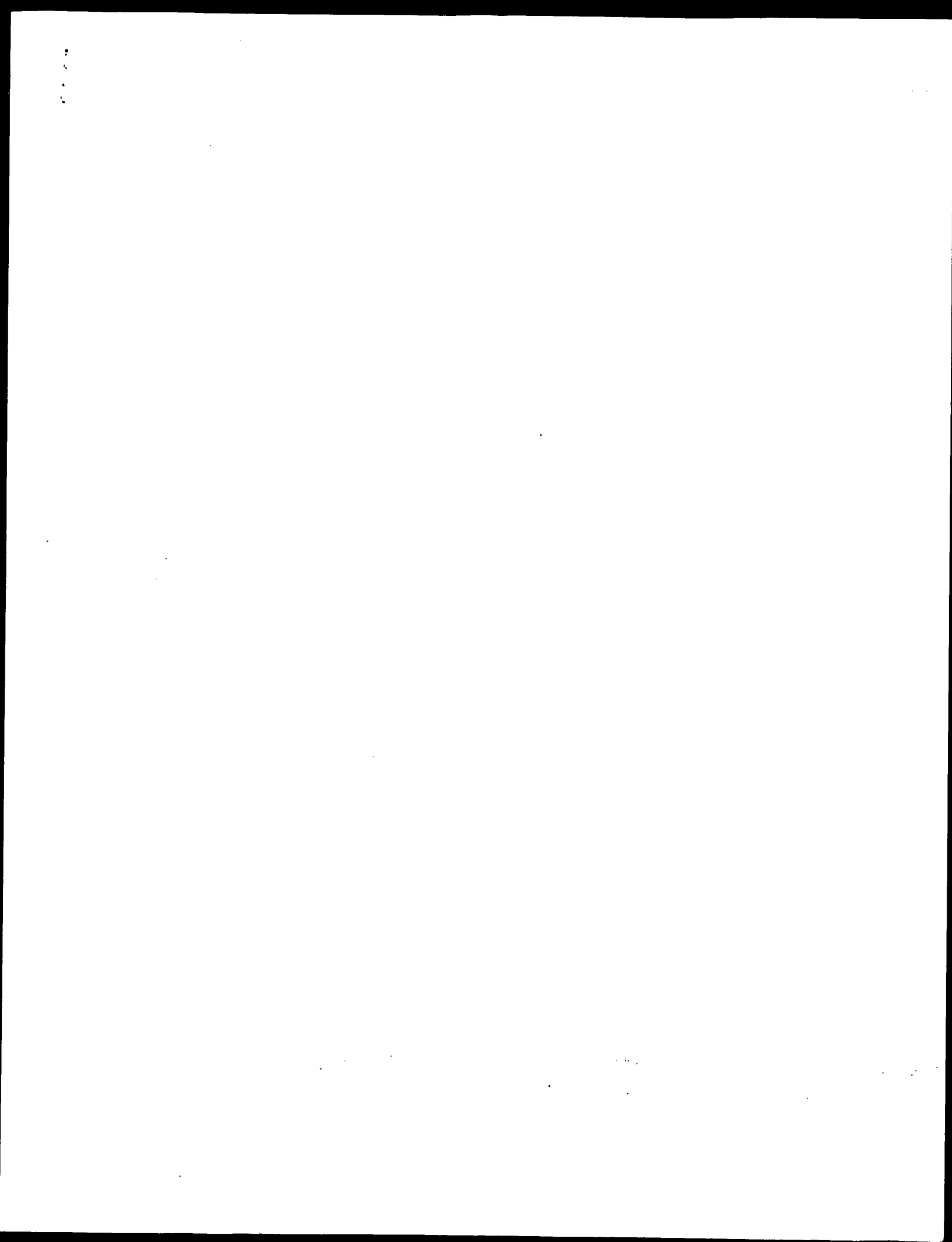
OY 2 AAATTAATACGACTCCTACTATAGGAGAC 29
DB 2 AAATTAATACGACTCCTACTATAGGAGAC 29

RESULT 15
US-09-953-321-15
Sequence 15, Application US/09953321
Patent No. US20020115083A1
GENERAL INFORMATION:
APPLICANT: PLOCKHOF, ANDREAS
APPLICANT: HANES, JOZEF
APPLICANT: JERMOTUS, LOTZ
TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
FILE REFERENCE: PLOCK/1 CON2
CURRENT APPLICATION NUMBER: US/09/953,321
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/425,585
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide T7B
US-09-953-321-15

Query Match 51.9%; Score 28; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAATTAATACGACTCCTACTATAGGAGAC 29
DB 6 AAATTAATACGACTCCTACTATAGGAGAC 33

Search completed: December 21, 2002, 19:28:10
Job time : 40.1306 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 ; Search time 16.9469 Seconds
(without alignments)
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Title: US-09-121-239-5
Sequence: 1 GACCACTCGTGTGAACTCA 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.4	55.8	95	US-10-025-380-53	Sequence 53, Appl
C 2	13.4	55.8	95	US-09-922-217-53	Sequence 53, Appl
C 3	13.4	55.8	95	US-09-833-263-53	Sequence 53, Appl
C 4	13.2	55.0	30	US-09-811-367B-17	Sequence 17, Appl
C 5	13.2	55.0	31	US-09-811-367B-16	Sequence 16, Appl
C 6	13.2	55.0	32	US-09-894-633A-50	Sequence 50, Appl
C 7	13.2	55.0	20	US-09-895-382-17	Sequence 17, Appl
C 8	13.2	55.0	35	US-09-780-929-115	Sequence 115, Appl
C 9	12.8	53.3	77	US-09-878-574-10313	Sequence 10313, A
C 10	12.8	53.3	86	US-10-040-497-57	Sequence 57, Appl
C 11	12.8	53.3	91	US-09-864-761-33030	Sequence 33030, A
C 12	12.6	52.5	48	US-09-864-785-3282	Sequence 3282, Ap
C 13	12.6	52.5	78	US-09-864-761-32336	Sequence 32336, A
C 14	12.4	51.7	22	US-08-983-605-347	Sequence 347, Appl
C 15	12.4	51.7	24	US-09-966-880A-20	Sequence 20, Appl
C 16	12.4	51.7	32	US-09-925-664-39	Sequence 39, Appl
C 17	12.4	51.7	32	US-09-921-992-63	Sequence 63, Appl
C 18	12.4	51.7	32	US-09-987-025-11	Sequence 11, Appl
C 19	12.2	50.8	57	US-10-153-064-82	Sequence 82, Appl

C 20	12.2	50.8	58	US-10-153-064-10	Sequence 10, Appl
C 21	12.2	50.8	58	US-10-153-064-83	Sequence 83, Appl
C 22	12.2	50.8	59	US-10-153-064-11	Sequence 11, Appl
C 23	12.2	50.0	24	US-09-905-291A-129	Sequence 129, Appl
C 24	12.2	50.0	24	US-09-220-920-77	Sequence 77, Appl
C 25	12.2	50.0	24	US-09-909-320-129	Sequence 129, Appl
C 26	12.2	50.0	24	US-09-909-088B-129	Sequence 129, Appl
C 27	12.2	50.0	24	US-09-565-233-16	Sequence 16, Appl
C 28	12.2	50.0	48	US-09-864-785-3011	Sequence 3011, Appl
C 29	12.2	50.0	48	US-09-864-785-3173	Sequence 3173, Ap
C 30	12.2	50.0	48	US-09-864-785-3203	Sequence 3203, Ap
C 31	12.2	50.0	48	US-09-864-785-3267	Sequence 3267, Ap
C 32	12.2	50.0	63	US-09-745-605-41	Sequence 41, Appl
C 33	12.2	50.0	73	US-09-888-280-53	Sequence 53, Appl
C 34	12.2	50.0	86	US-09-878-574-14526	Sequence 14526, A
C 35	12.2	50.0	100	US-09-878-446-997	Sequence 997, Appl
C 36	11.8	49.2	25	US-09-866-108-5107	Sequence 5107, Ap
C 37	11.8	49.2	25	US-09-866-108-5108	Sequence 5108, Ap
C 38	11.8	49.2	27	US-09-866-108-5109	Sequence 5109, Ap
C 39	11.8	49.2	10	US-09-829-004A-9	Sequence 9, Appl
C 40	11.8	49.2	31	US-09-753-436-8	Sequence 8, Appl
C 41	11.8	49.2	31	US-09-801-274-757	Sequence 757, Appl
C 42	11.8	49.2	32	US-09-882-246-58	Sequence 58, Appl
C 43	11.8	49.2	33	US-09-757-992-2	Sequence 2, Appl
C 44	11.8	49.2	37	US-09-882-246-25	Sequence 25, Appl
C 45	11.8	49.2	49	US-09-882-246-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-10-025-380-53/c
Sequence 53, Application US/10025380
Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.47C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 95
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 37, 60, 73, 76, 92
OTHER INFORMATION: n = A,T,C or G
US-10-025-380-53
Query Match 55.8%; Score 13.4; DB 9; Length 95;
Best Local Similarity 73.9%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 ACCAAGCTGCTGTAAGTCA 24
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DB 28 AACACAAAGTGTCAAGAACTGCA 6

RESULT 2

US-09-922-217-53/c
; Sequence 53, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aljun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 37, 60, 73, 76, 92
; OTHER INFORMATION: n = A,T,C or G
US-09-922-217-53

Query Match 55.8%; Score 13.4; DB 10; Length 95;
Best Local Similarity 73.9%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 ACCAAGCTGCTGTAAGTCA 24
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DB 28 AACACAAAGTGTCAAGAACTGCA 6

RESULT 3

US-09-833-263-53/c
; Sequence 53, Application US/09833263
; Patent No. US2002010547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aljun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833.263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(95)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-53

Query Match 55.8%; Score 13.4; DB 10; Length 95;
Best Local Similarity 73.9%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 ACCAAGCTGCTGTAAGTCA 24
| |||| |||| |||| ||
DB 28 AACACAAAGTGTCAAGAACTGCA 6

RESULT 4

US-09-811-367B-17
; Sequence 17, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811.367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-811-367B-17

Query Match 55.0%; Score 13.2; DB 9; Length 30;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 AACTGCTGCTGAAGTCA 22
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DB 6 AACTGCTGCTGAAGTCA 23

RESULT 5

US-09-811-367B-16/c
; Sequence 16, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811.367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-811-367B-16

Query Match 55.0%; Score 13.2; DB 9; Length 31;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Patent No. US20020172962A1
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
TIERK, CRAIG
TITLE OF INVENTION: METHODS OF PRODUCING NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,497
FILING DATE: 07-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/748,697
FILING DATE: 13-NOVEMBER-1996
APPLICATION NUMBER: 08/442,062
FILING DATE: 16-MAY-1995
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX05/DC-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-040-497-57
Query Match 53.3%; Score 12.8; DB 9; Length 86;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 16; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 GACCAACTCGTGTGTAATCGA 24
DB 21 GACCAACUCCAUCCAGAAACGCA 44
RESULT 11
US-09-864-761-33030
Sequence 33030, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 33030
LENGTH: 91
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL078623.21
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
OTHER INFORMATION: EST_HUMAN HIT: A1201676.1, EVALUATE 1.10e+00
US-09-864-761-33030
Query Match 53.3%; Score 12.8; DB 10; Length 91;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ACCAACTCGTGTGTA 17
DB 26 ACCAACTCGTGTGTA 41
RESULT 12
US-09-864-785-3282
Sequence 3282, Application US/09864785
Patent No. US20020177568A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Slinchcomb, Dan
APPLICANT: Draper, Ken
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
FILE REFERENCE: 400/022 (RBH00-812-D)
CURRENT APPLICATION NUMBER: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3282
LENGTH: 48

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;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-761-3282

Query Match          52.5%; Score 12.6; DB 9; Length 48;
Best Local Similarity 63.2%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 AACCTGTGTGTAACCTCC 23
    |||:|:| ||||:|
Db 2 AACCTGTGTGTAACCTCC 20

RESULT 13
US-09-864-761-32336/c
; Sequence 32336, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca.1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32336
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003677.1

;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
;; OTHER INFORMATION: NT HIT: AF096872.1, EVALUATE 2.40e+00
;; OTHER INFORMATION: EST_HUMAN HIT: R67876.1, EVALUATE 3.60e+00
US-09-864-761-32336

Query Match          52.5%; Score 12.6; DB 10; Length 78;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 ACTGTGTGTGTAACCTCCA 24
    |||:|:| ||||:|
Db 44 ACTGTGTGTGTAACCTCCA 26

RESULT 14
US-08-983-605-347/c
; Sequence 347, Application US/08983605A
; Patent No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; FILE REFERENCE: 2936.10400
; CURRENT FILING DATE: 1998-05-01
; EARLIER FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 347
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-347

Query Match          51.7%; Score 12.4; DB 8; Length 22;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TCGTGTGTGAACT 21
    |||:|:| ||||:|
Db 15 TCGTGTGTGAACT 2

RESULT 15
US-09-966-880A-20/c
; Sequence 20, Application US/09966880A
; Patent No. US2002016473A1
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Muramatsu, Masamichi
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
; FILE REFERENCE: 06501-088001
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/966,880A
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: PCT/JP00/01918
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: JP 11-371382
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP 11-178999
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: JP 11-87192
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence, p3
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 ; Search time 17.6531 Seconds
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562.024 Million cell updates/sec

Title: US-09-121-239-9
Perfect score: 25
Sequence: 1 GACTGTCACAGCATTCGCGTGACC 25

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCR_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	64.0	28	10	US-09-779-881-2
2	15.6	62.4	82	10	US-09-864-761-26163
3	14.4	57.6	100	10	US-09-983-965-1713
4	14	56.0	16	10	US-09-068-817-9
5	14	56.0	100	10	US-09-864-761-26368
6	13.8	55.2	34	10	US-09-772-120-4
7	13.8	55.2	80	10	US-09-864-761-21132
8	13.8	55.2	80	10	US-09-783-590-6697
9	13.8	55.2	89	10	US-09-741-669-78
10	13.2	52.8	77	10	US-09-815-242-2240
11	13	52.0	22	12	US-10-028-415-38
12	13	52.0	66	10	US-09-766-113-20
13	13	51.2	21	10	US-09-104-654-8
14	12.8	51.2	39	9	US-09-733-042-48
15	12.8	51.2	65	10	US-09-783-590-6219
16	12.8	51.2	94	10	US-09-294-0938-3985
17	12.8	51.2	96	10	US-09-864-761-23371
18	12.8	51.2	97	10	US-09-864-761-19961
19	12.6	50.4	29	10	US-09-828-303-49

20	12.6	50.4	67	10	US-09-783-590-1116	Sequence 1116, Ap
21	12.6	50.4	90	12	US-10-051-843-7	Sequence 7, Appl
22	12.4	49.6	25	10	US-09-866-108-13884	Sequence 13884, A
23	12.4	49.6	25	10	US-09-866-108-13885	Sequence 13885, A
24	12.4	49.6	25	10	US-09-866-108-13886	Sequence 13886, A
25	12.4	49.6	25	10	US-09-866-108-13887	Sequence 13887, A
26	12.4	49.6	64	10	US-09-766-113-4	Sequence 4, Appl
27	12.4	49.6	75	10	US-09-983-965-5804	Sequence 5804, Ap
28	12.4	49.6	90	10	US-09-917-330-3	Sequence 3, Appl
29	12.4	49.6	96	10	US-09-864-761-17593	Sequence 17593, A
30	12.2	48.8	17	10	US-09-866-108-10265	Sequence 10265, A
31	12.2	48.8	25	10	US-09-866-108-15157	Sequence 15157, A
32	12.2	48.8	25	10	US-09-866-108-15158	Sequence 15158, A
33	12.2	48.8	25	10	US-09-866-108-15159	Sequence 15159, A
34	12.2	48.8	25	10	US-09-866-108-15160	Sequence 15160, A
35	12.2	48.8	25	10	US-09-866-108-15161	Sequence 15161, A
36	12.2	48.8	25	10	US-09-866-108-15162	Sequence 15162, A
37	12.2	48.8	25	10	US-09-866-108-15163	Sequence 15163, A
38	12.2	48.8	25	10	US-09-866-108-15164	Sequence 15164, A
39	12.2	48.8	25	10	US-09-866-108-15165	Sequence 15165, A
40	12.2	48.8	30	10	US-09-752-110A-21	Sequence 21, Appl
41	12.2	48.8	47	10	US-09-264-468B-5	Sequence 4, Appl
42	12.2	48.8	66	10	US-09-572-365-6	Sequence 6, Appl
43	12.2	48.8	66	10	US-09-572-366-6	Sequence 6, Appl
44	12.2	48.8	66	10	US-09-573-465-6	Sequence 6, Appl
45	12.2	48.8	85	10	US-09-864-761-30027	Sequence 30027, A

ALIGNMENTS

RESULT 1
US-09-779-881-2/c
Sequence 2, Application US/09779881
Patent No. US20020081749A1
GENERAL INFORMATION:
APPLICANT: Kunitama, Sakari
APPLICANT: Aia Kieme, Timo
APPLICANT: Eskola, Jariko
TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED
FILE REFERENCE: TUR-080
CURRENT APPLICATION NUMBER: US/09/779,881
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/341,955
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/F198/00114
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide containing an amino group
US-09-779-881-2
Query Match 64.0% Score 16; DB 10; Length 28;
Best Local Similarity 100.0% Pred No. 73;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 28 CAGCATTCGCGTGACC 13
QY 10 CAGCATTCGCGTGACC 25
Db 28 CAGCATTCGCGTGACC 13
RESULT 2
US-09-864-761-26163/c
Sequence 26163, Application US/09864761
Patent No. US20020048763A1

```

; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26163
; LENGTH: 82
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AI031588.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.5
; OTHER INFORMATION: NT HTT: g111418318, EVALUO 4.00e-24
; OTHER INFORMATION: EST_HUMAN HIT: BF589388.1, EVALUO 5.00e-24
US-09-864-761-26163

Query Match          62.4%; Score 15.6; DB 10; Length 82;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 2 ACTGTCACAGCATTCCGCTGA 23
Db 50 ACTGTCACAGCACCCTCGTTA 29
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RESULT 3

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US-09-983-965-1713/c
; Sequence 1713, Application US/09983965
; Patent No. US200201377160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1713
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 56-LIB2809-014-01-E1-F8
US-09-983-965-1713

Query Match          57.6%; Score 14.4; DB 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 GACTGTCCACAGATTCGCTGAC 24
Db 51 GAATGCCACACCATGTGCTGCC 28
```

RESULT 4

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US-09-068-817-9
; Sequence 9, Application US/09068817
; Patent No. US20020081733A1
; GENERAL INFORMATION:
; APPLICANT: VeriAlife, C.M.
; APPLICANT: Mcivor, R.S.
; APPLICANT: Zhai, R.C.
; TITLE OF INVENTION: Method to prepare drug-resistant, non-malignant hematopoietic
; FILE REFERENCE: 600.347US2
; CURRENT APPLICATION NUMBER: US/09/068,817
; CURRENT FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/US96/18273
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: US 60/006,692
; PRIOR FILING DATE: 1995-11-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-068-817-9

Query Match          56.0%; Score 14; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GACTGTCCACAGCA 14
Db 3 GACTGTCCACAGCA 16
```

RESULT 5

```

US-09-864-761-26368
; Sequence 26368, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
```

```

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY FILING DATE: 2000-02-04 US 60/180,312
PRIORITY FILING DATE: 2000-05-26 US 60/207,456
PRIORITY FILING DATE: 2000-08-03 US 09/632,366
PRIORITY FILING DATE: 2000-10-04 GB 24263.6
PRIORITY FILING DATE: 2000-09-27 US 60/236,359
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30 PCT/US01/00673
PRIORITY FILING DATE: 2000-09-21 US 60/234,687
PRIORITY FILING DATE: 2000-06-30 US 09/608,408
PRIORITY FILING DATE: 2001-01-29 US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 26368
LENGTH: 100
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL022327.17
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.3
OTHER INFORMATION: NT HIT: g111432956, EVALUATE 3.00e-03
OTHER INFORMATION: EST_HUMAN HIT: BE348229.1, EVALUATE 2.00e-05
US-09-864-761-26368
Query Match 56.0%; Score 14; DB 10; Length 100;
Best Local Similarity 77.3%; Pred. No. 7.7e+02;
Matches 17; conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ACTGTCACACAGCATTCGCGTGA 23
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DB 20 ACTGACACACACGACACCCCTGCTGA 41

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RESULT 6
US-09-772-120-4
: Sequence 4, Application US/09772120
: Patent No. US20010014328A1
GENERAL INFORMATION:
APPLICANT: Deo, Yashwant M.
Kiefer, Tilhor
Graziano, Robert
TITLE OF INVENTION: Therapeutic Multispecific Compounds
Comprised of Anti-Fc
[SYMBOL. 97 \f "Symbol"] Receptor Antibodies
:
:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772.120
FILING DATE: 26-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,011
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MX1-064CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..36
OTHER INFORMATION: /note= "PCR primer"
:
:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-772-120-4
Query Match 55.2%; Score 13.8; DB 10; Length 34;
Best Local Similarity 72.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 GACGTGCACAGCATTCGCGTGACC 25
11111 | 11111 11111
Db 1 GACTGGATCGCAGCATTCAGCTGACC 25
RESULT 7
US-09-864-761-21132/c
: Sequence 21132, Application US/09864761
: Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-x-1

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; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21132
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012122.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: 914758563, EVALUATE 3.00e-06
; OTHER INFORMATION: EST_HUMAN HIT: AW293349.1, EVALUATE 4.00e-33
; OTHER INFORMATION: SWISSPROT HIT: P35820, EVALUATE 5.40e+00
US-09-864-761-21132

Query Match      55.2%; Score 13.8; DB 10; Length 80;
Best Local Similarity 72.0%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 GACTGTCACAGCATTCGGCTGAC 25
DB      68 GCCTCTCTCAGCCATCAGCTGATC 44

RESULT 8
US-09-783-590-6697/c
; Sequence 6697, Application US/09783590
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; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6697
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (72)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6697

Query Match      55.2%; Score 13.8; DB 10; Length 80;
Best Local Similarity 88.2%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GTCACAGCATTCGCT 21
DB      62 GTCACAGCATTCGCT 46

RESULT 9
US-09-741-669-78/c
; Sequence 78, Application US/09741669
; Patent No. US2002022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-741-669-78

Query Match      55.2%; Score 13.8; DB 10; Length 89;
Best Local Similarity 88.2%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CCACAGCATTCGCTGA 23
DB      88 CCACAGCATTCGCTGA 72

RESULT 10
US-09-815-242-2240
```



```
Sequence 2240, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trevelick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
CURRENT FILING DATE: 2001-03-21
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2240
LENGTH: 77
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-815-242-2240

Query Match      52.8%; Score 13.2; DB 10; Length 77;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 TGTCACAGACATTCGGCT 21
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DB      44 TGTCACGCAATGCGCT 61

RESULT 11
US-10-028-415-38/c
Sequence 38, Application US/10028415
Patent No. US20020151063A1
GENERAL INFORMATION:
APPLICANT: Lasham, Annette
APPLICANT: Watson, James D.
TITLE OF INVENTION: Methods for Modulating Apoptotic Cell
FILE OF INVENTION: Death
FILE REFERENCE: 11000.1004c3
CURRENT FILING DATE: 2001-12-20
CURRENT APPLICATION NUMBER: PCT/NZ01/00286
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 09/724,809
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/036,004
PRIOR FILING DATE: 1998-03-04
PRIOR APPLICATION NUMBER: US 08/713,557
PRIOR FILING DATE: 1996-08-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 22
TYPE: DNA
ORGANISM: Human
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US-10-028-415-38
Query Match      52.0%; Score 13; DB 12; Length 22;
Best Local Similarity 76.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      5 GTCCACAGACATTCGCTGACC 25
      ||| ||| ||| ||| |||
DB      22 GCCACAGACATTCGCTGCC 2

RESULT 12
US-09-766-113-20
Sequence 20, Application US/09766113
Patent No. US20010047525A1
GENERAL INFORMATION:
APPLICANT: Bruce, Wesley B.
APPLICANT: Niu, Xiping
TITLE OF INVENTION: No. US20010047525A1 Root-Preferred Promoter Elements
FILE OF INVENTION: and Methods of Use
FILE REFERENCE: 1166
CURRENT FILING DATE: 2001-01-19
CURRENT APPLICATION NUMBER: US 60/177,473
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 66
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic sequences flanking a random
OTHER INFORMATION: oligonucleotide
US-09-766-113-20

Query Match      52.0%; Score 13; DB 10; Length 66;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 ACTGTCCACAGACATTCGCTG 22
      ||||| ||| ||| |||
DB      46 ACTGTCTACGAAATTCAGCTG 66

RESULT 13
US-09-104-654-8/c
Sequence 8, Application US/09104654
Patent No. US2001008026A1
GENERAL INFORMATION:
APPLICANT: Schneider, Michael D.
APPLICANT: Overbeek, Paul
APPLICANT: Frenkel, Peter
TITLE OF INVENTION: System for Tissue-Restricted Gene
FILE OF INVENTION: Recombination
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,654
FILING DATE: 25-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
```

NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02973
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8810
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-104-654-8

Query Match 51.2%; Score 12.8; DB 10; Length 21;
Best Local Similarity 87.5%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TCACAGCATTCGCT 21
| | | | | | | | | |
Db 19 TCACACATTCGCT 4

RESULT 14
US-09-733-042-48/c
Sequence 48, Application US/09733042
Patent No. US20020168709A1
GENERAL INFORMATION:
APPLICANT: Hennecke, Frank
TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
FILE REFERENCE: 1700.0100001
CURRENT APPLICATION NUMBER: US/09/733,042
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/169,988
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 48
LENGTH: 39
TYPE: DNA
ORGANISM: 5'SV40 PUR
US-09-733-042-48

Query Match 51.2%; Score 12.8; DB 9; Length 39;
Best Local Similarity 70.8%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GACTGTCACAGCATTCGCTGAC 24
| | | | | | | | | | | | | | | | | | | | | |
Db 36 GACTTTCACACCTACGCGGCC 13

RESULT 15
US-09-783-590-6219/c
Sequence 6219, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21

NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6219
LENGTH: 65
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (45)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6219

Query Match 51.2%; Score 12.8; DB 10; Length 65;
Best Local Similarity 68.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GACTGTCACAGCATTCGCTGACC 25
| | | | | | | | | | | | | | | | | | | | | |
Db 38 GTCATCAACAGCATTCGCGCAAC 14

Search completed: December 21, 2002, 19:28:13
Job time: 18.6531 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 (Search time 14.1224 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-13

Sequence: 1 CAAGAGCAGCGAAGAGG 20

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Gapop 10.0, Gapext 1.0

Searched: 356696 seqs, 198428768 residues

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- 14: /cg2_6/ptodata/2/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	96	12	US-10-078-777-8
2	15.2	76.0	23	10	US-09-814-777A-82
3	14.8	74.0	84	12	US-10-078-777-7
4	14.8	74.0	87	12	US-10-078-777-9
5	14.2	71.0	45	12	US-10-002-278-14
6	14.2	71.0	91	10	US-09-864-761-19573
7	13.8	69.0	31	10	US-09-801-274-1776
8	13.8	69.0	84	10	US-09-864-761-26118
9	13.6	68.0	89	10	US-09-772-719-42
10	13.2	66.0	23	9	US-09-966-546-52
11	13.2	66.0	23	9	US-09-966-546-52
12	13.2	66.0	59	10	US-09-426-548-84
13	13.2	66.0	87	10	US-09-864-761-21662
14	12.8	64.0	19	9	US-09-963-875-14
15	12.8	64.0	21	10	US-09-918-203-3
16	12.8	64.0	32	10	US-09-885-478-20
17	12.8	64.0	32	10	US-09-885-478-21
18	12.8	64.0	97	10	US-09-864-761-19704
19	12.6	63.0	24	10	US-09-754-997A-41

20	12.6	63.0	43	9	US-10-027-806-90	Sequence 90, Appl
21	12.6	63.0	75	10	US-09-864-761-23841	Sequence 23841, A
22	12.6	63.0	94	10	US-09-864-761-22644	Sequence 22644, A
23	12.6	63.0	97	10	US-09-864-761-24367	Sequence 24367, A
24	12.4	62.0	18	10	US-09-789-556A-32	Sequence 32, Appl
25	12.4	62.0	20	10	US-09-789-556A-31	Sequence 31, Appl
26	12.4	62.0	22	10	US-09-789-556A-30	Sequence 30, Appl
27	12.4	62.0	26	10	US-09-789-556A-29	Sequence 29, Appl
28	12.4	62.0	31	10	US-09-801-274-1190	Sequence 1190, Appl
29	12.4	62.0	38	12	US-09-864-761-1767	Sequence 48, Appl
30	12.4	62.0	80	10	US-09-864-761-1767	Sequence 48, Appl
31	12.2	61.0	21	10	US-09-955-380-13	Sequence 13, Appl
32	12.2	61.0	21	9	US-09-955-380-13	Sequence 48, Appl
33	12.2	61.0	30	9	US-10-033-297-48	Sequence 48, Appl
34	12.2	61.0	30	9	US-09-777-430A-3	Sequence 3, Appl1
35	12.2	61.0	30	10	US-09-777-430A-4	Sequence 571, App
36	12.2	61.0	31	10	US-09-801-274-571	Sequence 8, Appl1
37	12.2	61.0	43	12	US-10-001-344-8	Sequence 2965, Ap
38	12.2	61.0	50	10	US-09-504-231A-2965	Sequence 2965, Ap
39	12.2	61.0	50	10	US-09-274-553D-2965	Sequence 1332, Ap
40	12.2	61.0	61	9	US-09-946-807-1332	Sequence 1332, Ap
41	12.2	61.0	61	10	US-09-795-668-1332	Sequence 1332, Ap
42	12.2	61.0	61	10	US-09-795-668-1332	Sequence 1332, Ap
43	12.2	61.0	78	10	US-09-864-761-24659	Sequence 24659, A
44	12.2	61.0	90	10	US-09-864-761-28450	Sequence 28450, A
45	12.2	61.0	91	10	US-09-783-590-2439	Sequence 2439, Ap

ALIGNMENTS

RESULT 1
US-10-078-777-8
Sequence 8, Application US/10078777
Patent No. US2002013785A1
GENERAL INFORMATION:
APPLICANT: REDEI, Eva
TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF
FILE REFERENCE: 0054-103
CURRENT APPLICATION NUMBER: US/10/078,777
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/366,627
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 08/523,125
PRIOR FILING DATE: 1995-09-08
PRIOR APPLICATION NUMBER: 08/304,383
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 8
LENGTH: 96
TYPE: DNA
ORGANISM: Homo sapiens
US-10-078-777-8
Query Match 87.0%; Score 17.4; DB 12; Length 96;
Best local similarity 94.7%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 37 CAAGAGCAGCGAAGAGG 55
QY 1 CAAGAGCAGCGAAGAGG 19
|||||
Db 37 CAAGAGCAGCGAAGAGG 55
RESULT 2
US-09-814-777A-82
Sequence 82, Application US/09814777A
Patent No. US20020142415A1
GENERAL INFORMATION:
APPLICANT: KOOPMAN, Peter Anthony
APPLICANT: MOSCAT, George Eugene Orlando

	Query Match	76.0%;	Score 15.2;	DB 10;	Length 23;
	Best Local Similarity	85.0%;	Pred. No. 3e+02;		
Matches	17; Conservative	0;	Mismatches	3;	Indels 0; Gaps 0;
QY	1 CAAGGACGCGGCAAGAAGG	20			
Dd	2 CADAAGCGGTGGGAAGAAGG	21			

```

RESULT 3
US-10-078-777-7
; Sequence 7, Application US/10078777
; Patent No. US20020157885A1
; GENERAL INFORMATION:
; APPLICANT: REDEL, Eva
; TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF
; FILE REFERENCE: 0054-1U3
; CURRENT APPLICATION NUMBER: US/10/078,777
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/366,627
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 08/523,125
; PRIOR FILING DATE: 1995-09-08
; PRIOR APPLICATION NUMBER: 08/304,383
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-078-777-7

```

Query Match	74.0%	Score 14.8;	DB 12;	Length 84;
Best Local Similarity	88.9%	Pred. No. 5e+02;		
Matches 16; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
1 CAAGGACGACGGGACAA	18			
Db 37 CAAGGAGCTGGGACAA	54			

RESULT 4
US-10-078-777-9
Sequence 9, Application US/10078777
Patent No. US20020137885A1
GENERAL INFORMATION:
APPLICANT: REDEL, Eva
APPLICANT: AIRD, Fraser
TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF
FILE REFERENCE: 0054-1U3
CURRENT APPLICATION NUMBER: US/10/078, 777
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/366,627

Query Match	74.0%;	Score 14.8;	DB 12;	Length 87;
Best Local Similarity	88.9%;	Pred. No. 5e+02;		
Matches	16;	Conservative	0;	Mismatches 2;
				Indels 0;
				Gaps 0;
OY	1	CAAAAGACGACGGAGAA	18	
Db	37	CAAAAGACCTGGAGAA	54	

```

RESULT 5
US-10-002-278-14/c
; Sequence 14, Application US/10002278
; Patent No. US20020132334A1
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M.
APPLICANT: Basler, Ronald
APPLICANT: Yamada, Toshiya
TITLE OF INVENTION: CLOTHING
FILE REFERENCE: 0575/40314-A
CURRENT APPLICATION NUMBER: US/10/002,278
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Fragment encoding dorsalIn-1 N-terminus
NAME/KEY: primer.bldd
LOCATION: (1) - (45)
OTHER INFORMATION:
US-10-002-278-14

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```

Query Match      71.0%      Score 14.2; DB 12; Length 45;
Best Local Similarity 84.2%      Pred No 8.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAAAGGACGCGGAGAAAG 19
      || |||||
Db      35 CATAGGACGCGAGCAGAG 17

```

RESULT 6
 US-09-864-761-19573
 : Sequence 19573, Application US/09864761
 : Patent No. US20020048763A1
 : GENERAL INFORMATION:
 : APPLICANT: Penn, Sharon G.
 : APPLICANT: Rank, David R.
 : APPLICANT: Hanzel, David K.
 : APPLICANT: Chen, Wensheng
 : TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 : TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 : FILE REFERENCE: Aeomica-x-1
 : CURRENT APPLICATION NUMBER: US/09/864,761
 : CURRENT FILING DATE: 2001-05-23
 : PRIOR APPLICATION NUMBER: US 60/180,312
 : PRIOR FILING DATE: 2000-02-04
 : PRIOR APPLICATION NUMBER: US 60/207,456

```

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19573
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011416.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
; OTHER INFORMATION: NT HIT: X94232.1, EVALUATE 1.60e-01
; US-09-864-761-19573

Query Match          71.0%; Score 14.2; DB 10; Length 91;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAAAGAGCAGGAGGAGAG 19
DB      49 CAGAGCAGCAGCAGCAGAG 67

RESULT 7
US-09-801-274-1776/c
; Sequence 1776, Application US/09801274
; GENERAL INFORMATION:
; APPLICANT: Carilli, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
```

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; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1776
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-274-1776

Query Match          69.0%; Score 13.8; DB 10; Length 31;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGCAGCAGGAGGAGAGC 20
DB      31 AAAGCAGCAGCAGGAGAG 13

RESULT 8
US-09-864-761-26118
; Sequence 26118, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Bank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
```

SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 26118
LENGTH: 84
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL022318.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 43
OTHER INFORMATION: EXPRESSED IN HETAL, SIGNAL = 8.6
OTHER INFORMATION: NT HIT: AL163210.2, EVALU2 2.00e-35
OTHER INFORMATION: EST_HUMAN HIT: BE150340.1, EVALU2 1.00e-34
US-09-864-761-26118

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 10; Length 84;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 AGAGACGAGGAGAGAG 20
DB 56 AGAGACGAGGAGAGAG 72

RESULT 9
US-09-772-719-42

Sequence 42, Application US/09772719
Patent No. US20020137910A1

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 369 Pine Street

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/772,719

FILING DATE: 30-JAN-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,049

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3E

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034

TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 89 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 4th MN intron
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-772-719-42

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 10; Length 89;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CAAGAGCGGAGGAGAG 20
DB 27 CAAGAGCGGCGGCGAGG 46

RESULT 10
US-09-966-546-52

Sequence 52, Application US/09966546
Patent No. US20020168716A1

GENERAL INFORMATION:

APPLICANT: Fernandes, Elma

APPLICANT: Vernet, Corine

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: Them

FILE REFERENCE: Cura-46 (15966-546)

CURRENT APPLICATION NUMBER: US/09/966,546

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/544,511

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 52

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Oligo Primer

US-09-966-546-52

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 9; Length 23;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGCGGAGGAGAG 19
DB 1 AAAGGCGGAGGAGAGAG 18

RESULT 11
US-09-966-545-52

Sequence 52, Application US/09966545
Patent No. US20020172999A1

GENERAL INFORMATION:

APPLICANT: Fernandes, Elma

APPLICANT: Vernet, Corine

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: No. US20020172999A1 Human Proteins and Polynucleotides Encod

FILE REFERENCE: Cura-46 (15966-546)

CURRENT APPLICATION NUMBER: US/09/966,545

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/544,511

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 52

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Oligo Primer

US-09-966-545-52

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Query Match      66.0%; Score 13.2; DB 9; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 AAAGGCGGAGGAGGAGG 19
      1 AAAGGCGGAGGAGGAGG 18

Db

RESULT 12
US-09-426-548-84/c
; Sequence 84, Application US/09426548
; Patent No. US20010044936A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, David
; APPLICANT: Lin, Goerke, Jull L.
; TITLE OF INVENTION: No. US20010044936A1 Mutations in Human MLH1 and MSH2 Genes Used
; FILE REFERENCE: DEX-0054
; CURRENT APPLICATION NUMBER: US/09/426,548
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-426-548-84

Query Match      66.0%; Score 13.2; DB 10; Length 59;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 AAAGGCGGAGGAGGAGG 19
      46 AAAGGCGGAGGAGGAGG 29

Db

RESULT 13
US-09-864-761-21662
; Sequence 21662, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21662
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL034399.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HB1100, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EST HUMAN HIT: BF337932.1, EVALUATE 2.70e-01
US-09-864-761-21662

Query Match      66.0%; Score 13.2; DB 10; Length 87;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1 CAAGGAGGAGGAGGAGG 18
      19 CTAAGGAGGAGGAGGAGG 36

Db

RESULT 14
US-09-963-875-14
; Sequence 14, Application US/09963875
; Patent No. US20020164307A1
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treati
; FILE REFERENCE: 1763/1235
; CURRENT APPLICATION NUMBER: US/09/963,875
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US60/169082
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/215109
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/238880
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/731261
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: oligonucleotide
US-09-963-875-14

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGAGCGAGGAG 16
|| |||||
DB 3 CACTGAGCGAGGAG 18

RESULT 15

US-09-918-203-3/c
; Sequence 3, Application US/09918203
; Patent No. US2002002530A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Affourtit, Jason
; APPLICANT: Seymour, Albert
; TITLE OF INVENTION: A PCR-BASED MULTIPLEX ASSAY FOR DETERMINING HAPLOTYPE
; FILE REFERENCE: PC10704DAM
; CURRENT APPLICATION NUMBER: US/09/918,203
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-203-3

Query Match 64.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGCAGGAGGAGG 20
||| |||||
DB 21 GGAGCAGGAGGATG 6

Search completed: December 21, 2002, 19:28:15
Job time : 16.1224 secs

Mon Dec 23 08:47:56 2002

us-09-121-239-16.rnpb

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 (Search time 16.9469 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-16
Perfect score: 24
Sequence: 1 GTGGACATGATGACCCCTTCAGCGG 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	65.0	95	10 US-09-864-761-29032	Sequence 29032, A
2	15.2	63.3	61	9 US-09-946-807-1334	Sequence 1334, Ap
3	15.2	63.3	61	10 US-09-795-668-1334	Sequence 1334, Ap
4	15.2	63.3	61	10 US-09-795-668-1334	Sequence 1334, Ap
5	14.6	60.8	38	9 US-09-792-793A-47	Sequence 47, Appl
6	14.2	59.2	31	10 US-09-801-274-652	Sequence 652, App
7	14	58.3	26	10 US-09-779-881-1	Sequence 1, Appl
8	14	58.3	32	10 US-09-263-589-57	Sequence 57, Appl
9	13.8	57.5	96	10 US-09-864-761-22792	Sequence 22792, A
10	13.6	56.7	40	10 US-09-828-366-26	Sequence 28, Appl
11	13.6	56.7	60	10 US-09-990-080-20	Sequence 20, Appl
12	13.6	55.8	65	10 US-09-783-590-2448	Sequence 2448, Ap
13	13.4	55.0	32	12 US-10-084-206-9	Sequence 9, Appl
14	13.2	55.0	82	10 US-09-923-876-1514	Sequence 1514, Ap
15	13	54.2	37	10 US-09-882-246-51	Sequence 51, Appl
16	13	54.2	43	9 US-09-978-295A-282	Sequence 282, App
17	13	54.2	43	9 US-09-978-697-282	Sequence 282, App
18	13	54.2	43	9 US-09-978-192A-282	Sequence 282, App
19	13	54.2	76	10 US-09-864-761-31800	Sequence 31800, A

ALIGNMENTS

20	13	54.2	79	10	US-09-864-761-26494	Sequence 26494, A
C 21	13	54.2	81	10	US-09-983-965-887	Sequence 887, App
C 22	12.8	53.3	18	9	US-09-942-596A-36	Sequence 36, Appl
C 22	12.8	53.3	18	10	US-09-942-596A-36	Sequence 36, Appl
C 24	12.8	53.3	18	10	US-09-764-420A-37	Sequence 37, Appl
C 25	12.8	53.3	31	10	US-09-801-274-183	Sequence 183, App
C 26	12.8	53.3	31	10	US-09-801-274-184	Sequence 184, App
C 27	12.8	53.3	39	9	US-09-925-922-10	Sequence 10, Appl
C 28	12.8	53.3	49	12	US-10-036-342-21	Sequence 21, Appl
C 29	12.6	52.5	39	10	US-09-263-959-222	Sequence 222, App
C 30	12.6	52.5	46	10	US-09-263-959-222	Sequence 145, App
C 31	12.6	52.5	46	9	US-09-853-526-253	Sequence 253, App
C 32	12.6	52.5	47	10	US-09-901-484A-253	Sequence 253, App
C 33	12.6	52.5	71	10	US-09-983-965-294	Sequence 294, App
C 34	12.6	52.5	79	10	US-09-333-527-32	Sequence 32, Appl
C 35	12.6	52.5	93	10	US-09-864-761-21892	Sequence 21892, A
C 36	12.4	51.7	25	10	US-09-866-108-12719	Sequence 12719, A
C 37	12.4	51.7	25	10	US-09-866-108-12720	Sequence 12720, A
C 38	12.4	51.7	25	10	US-09-866-108-12721	Sequence 12721, A
C 39	12.4	51.7	25	10	US-09-866-108-12722	Sequence 12722, A
C 40	12.4	51.7	31	10	US-09-801-274-226	Sequence 226, App
C 41	12.4	51.7	53	10	US-09-944-036-34	Sequence 34, Appl
C 42	12.4	51.7	53	10	US-09-944-036-36	Sequence 36, Appl
C 43	12.4	51.7	74	10	US-09-783-590-9244	Sequence 9244, Ap
C 44	12.4	51.7	88	9	US-09-971-980-16	Sequence 16, Appl
C 45	12.4	51.7	92	10	US-09-983-965-3542	Sequence 3542, Ap

RESULT 1
US-09-864-761-29032
Sequence 29032, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aomica-x-1
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29032
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121908.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: D17760.1, EVALUATE 7.90e-01
; OTHER INFORMATION: EST_HUMAN HIT: AW629605.1, EVALUATE 7.40e-02
; US-09-864-761-29032
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Query Match
Best Local Similarity 65.0%; Score 15.6; DB 10; Length 95;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1 GTGAACATGAAGCCCTTCAGC 22
51 GGGAGAGATGAAGCCCTTCATC 72
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RESULT 2
; US-09-946-807-1334
; Sequence 1334, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreln
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1334
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-946-807-1334
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Query Match
Best Local Similarity 63.3%; Score 15.2; DB 9; Length 61;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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37 TGAATATGAAGCATTCAG 56
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RESULT 3
; US-09-795-668-1334
; Sequence 1334, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
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; APPLICANT: Stefansson, Hreln
; APPLICANT: Steinhorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1334
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-795-668-1334
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Query Match
Best Local Similarity 63.3%; Score 15.2; DB 10; Length 61;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 2 TGAACATGAAGCCCTTCAG 21
37 TGAATATGAAGCATTCAG 56
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RESULT 4
; US-09-795-668-1334
; Sequence 1334, Application US/09795668
; Patent No. US2002004954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreln
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1334
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-795-668-1334
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Query Match
Best Local Similarity 63.3%; Score 15.2; DB 10; Length 61;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 2 TGAACATGAAGCCCTTCAG 21
37 TGAATATGAAGCATTCAG 56
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RESULT 5
; US-09-792-793A-47
; Sequence 47, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 38
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: forward primer (SDF-1-Beta)
US-09-792-793A-47
Query Match          60.8%; Score 14.6; DB 9; Length 38;
Best Local Similarity 81.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGGACATGAAGCCCTTCAGC 22
DB 7 TAGCATATGAAGCCCTTCAGC 27

RESULT 6
US-09-801-274-652
; Sequence 652, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825-2009-001
; CURRENT APPLICATION NUMBER: US/09/801/274
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 652
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-652

Query Match          59.2%; Score 14.2; DB 10; Length 31;
Best Local Similarity 76.2%; Pred. No. 5e+02;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGGACATGAAGCCCTTCAGC 22
DB 10 TGGACATGAAGCCCTTCAGC 30

RESULT 7
US-09-779-881-1/C
; Sequence 1, Application US/09779881
; Patent No. US20020081749A1
; GENERAL INFORMATION:
; APPLICANT: Kultima, Sakari
; APPLICANT: Ala-Kleme, Timo
; APPLICANT: Eskola, Jarkko
; APPLICANT: Koskela, Jukka
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED
; FILE REFERENCE: IOR-080
; CURRENT APPLICATION NUMBER: US/09/779,881
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US/09/723,411,955
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: PCT/FI98/00114
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO:
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide containing amino groups
US-09-779-881-1
Query Match          58.3%; Score 14; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 AAGCCCTTCAGCG 24
DB 26 AAGCCCTTCAGCG 13

RESULT 8
US-09-263-689-57
; Sequence 57, Application US/09263689
; Patent No. US20020150970A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/946,914
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-263-689-57

Query Match          58.3%; Score 14; DB 10; Length 32;
Best Local Similarity 77.3%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGACATGAAGCCCTTCAGCG 24
DB 8 GGCCCATCATGCGCTTCAGCG 29

RESULT 9
US-09-864-761-22792/C
; Sequence 22792, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
```

APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aegion-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 22792
LENGTH: 96
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC002458.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: NT HIT: D14547.1, EVALUATE 2.00e-10
OTHER INFORMATION: EST_HUMAN HIT: A1392964.1, EVALUATE 9.00e-17
US-09-864-761-22792

Query Match 58.3%; Score 14; DB 10; Length 96;
Best Local Similarity 77.3%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGACATGAGCCCTTCAGC 22
DB 82 GTGAACATAAAGGCTTCATC 61

RESULT 10
US-09-828-366-28
Sequence 28, Application US/09828366
Patent No. US20020010137A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Klein, Robert D.
APPLICANT: Napier, Mary
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC
FILE REFERENCE: P1694R1C1
CURRENT APPLICATION NUMBER: US/09/828,366
CURRENT FILING DATE: 2001-04-05
Prior filing data removed - refer to P16M or file wrapper
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 28
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-828-366-28

Query Match 57.5%; Score 13.8; DB 10; Length 40;
Best Local Similarity 88.2%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACATGAGCCCTTC A 20
DB 18 GAACATGAGCCCTTC A 34

RESULT 11
US-09-990-080-20
Sequence 20, Application US/09990080
Patent No. US20020102686A1
GENERAL INFORMATION:
APPLICANT: Morin, Gregg B.
APPLICANT: Genon Corporation
TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
FILE REFERENCE: 018/258c
CURRENT APPLICATION NUMBER: US/09/990,080
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 09/052,864
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 20
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: RT6 oligo
US-09-990-080-20

Query Match 56.7%; Score 13.6; DB 10; Length 60;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAACATGAGCCCTTCAGG 23
DB 21 GAACATGAGCCCTTCAGG 40

RESULT 12
US-09-783-590-2448/C
Sequence 2448, Application US/09783590
Patent No. US20020110850A1

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GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Steven A.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: P-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/783,590
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Perl Program
SEQ ID NO: 2448
LENGTH: 65
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 127
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-2448

Query Match      56.7%; Score 13.6; DB 10; Length 65;
Best Local Similarity 80.0%; Prod No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 54 GAACATGAAGCCCTTCAGCG 35

RESULT 13
US-10-084-206-9/C
Sequence 9, Application US/10084206
Patent No. US20020106741A1
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: G-Protein Receptor HTMD29
FILE REFERENCE: P191D1C1
CURRENT APPLICATION NUMBER: US/10/084,206
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/468,534
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 09/399,095
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentln Version 3.1
SEQ ID NO: 9
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Contains the cleavage site for the restriction
US-10-084-206-9

Query Match      55.8%; Score 13.4; DB 12; Length 32;
Best Local Similarity 73.9%; Prod. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 2 TGGACATGAAGCCCTTCAGCG 24
30 TGGAAATGAGAGCTTCAGCG 8

RESULT 14
US-09-923-876-1514/C

```

```

Sequence 1514, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: P-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO: 1514
LENGTH: 82
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700158952H1
NAME/KEY: unsure
LOCATION: 2, 12-13, 37, 51, 58, 65, 67, 81
OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-1514

Query Match      55.0%; Score 13.2; DB 10; Length 82;
Best Local Similarity 75.0%; Prod. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 28 GAACATGAAGCCCTTCAGCG 9

RESULT 15
US-09-883-246-51
Sequence 51, Application US/09882246
Patent No. US20020106652A1
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
WILLIS, MICHAEL
KOCH, TAD
RINGQUIST, STEVEN
JENSEN, KIRK
ATKINSON, BRENT
TITLE OF INVENTION: SYSTEMATIC EVOLUTION
OF
LIGANDS BY EXPONENTIAL
ENRICHMENT: PHOTOSELECTION
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/882,246
FILING DATE: 14-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,293
FILING DATE: <Unknown>

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APPLICATION NUMBER: PCT/US94/10542
FILING DATE: 18 September 1994
APPLICATION NUMBER: 08/123,935
FILING DATE: 17 September 1993
APPLICATION NUMBER: 08/143,564
FILING DATE: 25 October 1993
APPLICATION NUMBER: 07/714,131
FILING DATE: 10 JUNE 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11 JUNE 1990
APPLICATION NUMBER: 07/931,473
FILING DATE: 17 AUGUST 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/US-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-882-246-51

Query Match 54.2%; Score 13; DB 10; Length 37;
Best Local Similarity 61.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGGAACATGAGCCCTTCAG 21
I:|||||:|||||:
Db 3 GUGGAACCTCAATCCCGUAG 23

Search completed: December 21, 2002, 19:28:16
Job time: 17.9469 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 : Search time 19.0653 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-22

Sequence score: 27
1 TCTGACTTGAGCCTCAGGCTGACT 27

Scoring table: IDENTITY_NDC
Gapop 10.0, Capext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications, NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	81.5	22	10	US-09-995-912-4
C 2	14.8	54.8	67	10	US-09-974-300-4445
C 3	14.8	54.8	69	10	US-09-974-300-4378
C 4	14.8	54.8	69	10	US-09-974-300-4373
C 5	14.8	54.8	76	10	US-09-974-300-4374
C 6	14.8	54.8	76	10	US-09-974-300-4414
C 7	14.8	54.8	76	10	US-09-974-300-4426
C 8	14.8	54.8	76	10	US-09-974-300-4444
C 9	14.8	54.8	76	10	US-09-974-300-8449
C 10	14.8	54.8	76	10	US-09-974-300-8461
C 11	14.8	54.8	76	10	US-09-974-300-8477
C 12	14.8	54.8	76	10	US-09-974-300-8477
C 13	14.8	54.8	84	10	US-09-864-761-17329
C 14	14.8	54.8	87	10	US-09-864-761-19502
C 15	14.6	54.1	79	10	US-09-864-761-28857
C 16	14.4	53.3	36	10	US-09-504-231A-2483
C 17	14.4	53.3	36	10	US-09-504-231A-2660
C 18	14.4	53.3	36	10	US-09-504-231A-2816
C 19	14.4	53.3	36	10	US-09-274-553D-2483

C 20	14.4	53.3	36	10	US-09-274-553D-2660	Sequence 2660, Ap
C 21	14.4	53.3	36	10	US-09-274-553D-2816	Sequence 2816, Ap
C 22	14.2	52.6	96	12	US-10-078-777-8	Sequence 8, Appl
C 23	14	51.9	42	10	US-09-286-240-9	Sequence 353, App
C 24	14	51.9	42	10	US-09-765-272-353	Sequence 2517, Ap
C 25	13.8	51.1	36	10	US-09-504-231A-2517	Sequence 2517, Ap
C 26	13.8	51.1	36	10	US-09-504-231A-2514	Sequence 2514, Ap
C 27	13.8	51.1	36	10	US-09-504-231A-2740	Sequence 2740, Ap
C 28	13.8	51.1	36	10	US-09-504-231A-2807	Sequence 2807, Ap
C 29	13.8	51.1	36	10	US-09-504-231A-2815	Sequence 2815, Ap
C 30	13.8	51.1	36	10	US-09-504-231A-2830	Sequence 2830, Ap
C 31	13.8	51.1	36	10	US-09-504-231A-2879	Sequence 2879, Ap
C 32	13.8	51.1	36	10	US-09-274-553D-2517	Sequence 2517, Ap
C 33	13.8	51.1	36	10	US-09-274-553D-2534	Sequence 2534, Ap
C 34	13.8	51.1	36	10	US-09-274-553D-2740	Sequence 2740, Ap
C 35	13.8	51.1	36	10	US-09-274-553D-2807	Sequence 2807, Ap
C 36	13.8	51.1	36	10	US-09-274-553D-2815	Sequence 2815, Ap
C 37	13.8	51.1	36	10	US-09-274-553D-2830	Sequence 2830, Ap
C 38	13.8	51.1	36	10	US-09-274-553D-2879	Sequence 2879, Ap
C 39	13.8	51.1	36	10	US-09-864-761-26264	Sequence 26264, A
C 40	13.6	50.4	31	10	US-09-801-274-1152	Sequence 1152, Ap
C 41	13.4	49.6	36	10	US-09-504-231A-2080	Sequence 2080, Ap
C 42	13.4	49.6	36	10	US-09-504-231A-2279	Sequence 2279, Ap
C 43	13.4	49.6	36	10	US-09-504-231A-2515	Sequence 2515, Ap
C 44	13.4	49.6	36	10	US-09-504-231A-2709	Sequence 2709, Ap
C 45	13.4	49.6	36	10	US-09-274-553D-2090	Sequence 2090, Ap

ALIGNMENTS

RESULT 1
US-09-995-912-4/c
Sequence 4, Application US/0995912
Patent No. US20020137076A1
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
TITLE OF INVENTION: RNA Polymers and Uses Thereof
FILE REFERENCE: PRNG-06684
CURRENT APPLICATION NUMBER: US/09/995,912
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/253,451
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-995-912-4

Query Match 81.5%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTGCA 25
Db 22 GACTTGAGCCTCAGGCTGCA 1

RESULT 2
US-09-974-300-4445
Sequence 4445, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
Expression

FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4445
LENGTH: 67
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4445

Query Match 54.8%; Score 14.8; DB 10; Length 67;
Best Local Similarity 73.1%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGCTCTGAG 26
||||| | | | | | | |
Db 20 TCTGACTTTTATCATCAGAGGCTCGAAG 45

RESULT 3
US-09-974-300-4378
Sequence 4378, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4378
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4378

Query Match 54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 73.1%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGCTCTGAG 26
||||| | | | | | | |
Db 20 TCTGACTTTTATCATCAGAGGCTCGAAG 45

RESULT 4
US-09-974-300-4393
Sequence 4393, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4393
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4393

Query Match 54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 73.1%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGCTCTGAG 26
||||| | | | | | | |
Db 20 TCTGACTTTTATCATCAGAGGCTCGAAG 45

RESULT 5
US-09-974-300-4374
Sequence 4374, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4374
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4374

Query Match 54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGCTCTGAG 26
||||| | | | | | | |
Db 27 TCTGACTTTTATCATCAGAGGCTCGAAG 52

RESULT 6
US-09-974-300-4414
Sequence 4414, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4414
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4414


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Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGAGGCTGTGAG 26
    |||||
DB 27 TCTGACTTTTAAATCAGAGGCTCGAAG 52

RESULT 7
US-09-974-300-4426
; Sequence 4426, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4426
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-4426

Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGAGGCTGTGAG 26
    |||||
DB 27 TCTGACTTTTAAATCAGAGGCTCGAAG 52

RESULT 8
US-09-974-300-4444
; Sequence 4444, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4444
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-4444

Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGAGGCTGTGAG 26
    |||||
DB 27 TCTGACTTTTAAATCAGAGGCTCGAAG 52

Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGAGGCTGTGAG 26
    |||||
DB 27 TCTGACTTTTAAATCAGAGGCTCGAAG 52

RESULT 9
US-09-974-300-8409
; Sequence 8409, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8409
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-8409

Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGAGGCTGTGAG 26
    |||||
DB 27 TCTGACTTTTAAATCAGAGGCTCGAAG 52

RESULT 10
US-09-974-300-8449
; Sequence 8449, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8449
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-8449

Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGAGGCTGTGAG 26
    |||||
DB 27 TCTGACTTTTAAATCAGAGGCTCGAAG 52

RESULT 11
US-09-974-300-8461
; Sequence 8461, Application US/09974300
; Patent No. US20020146721A1
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RESULT 14
US-09-864-761-19502
; Sequence 19502, Application US/09864761

```

Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aesomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIORITY FILING DATE: 2001-05-23
PRIORITY FILING DATE: 2000-02-04
PRIORITY FILING DATE: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY FILING DATE: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY FILING DATE: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY FILING DATE: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY FILING DATE: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY FILING DATE: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY FILING DATE: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY FILING DATE: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY FILING DATE: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY FILING DATE: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
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PRIORITY FILING DATE: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY FILING DATE: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY FILING DATE: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY FILING DATE: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY FILING DATE: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 19502
LENGTH: 87
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009421.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN B747, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN HEL10, SIGNAL = 2.7
OTHER INFORMATION: EST_HUMAN HIT: H15308.1, EVALUATE 2.00e-20
OTHER INFORMATION: NT_HIT: AL163248.2, EVALUATE 5.00e-14
US-09-864-761-19502
Query Match 54.8%; Score 14.8; DB 10; Length 87;
Best Local Similarity 73.1%; Fred.No.8.4e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Mon Dec 23 08:47:58 2002

us-09-121-239-22.rnpb

Page 6

Query Match	54.1%	Score 14.6	DB 10	Length 79
Best Local Similarity	81.0%	Pred. No. 1e+03		
Matches 17	Conservative	0	Mismatches 4	Indels 0
				Gaps 0
QY	5	ACTTGGACGCTCAGGCTCTGA	25	
Db	50	ACTTGGACGCTCAGGCTCTGA	30	

Search completed: December 21, 2002, 19:28:18
Job time : 21.0653 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 [Search time 19.0653 Seconds
(without alignments)
562.024 Million cell updates/sec]

Title: US-09-121-239-23
Perfect score: 27
Sequence: 1 UCUGACUUGAGCCUCCAGGUCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 35696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCRN_NMW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	81.5	22	10	US-09-995-912-4
2	14.8	54.8	67	10	US-09-974-300-4445
3	14.8	54.8	69	10	US-09-974-300-4378
4	14.8	54.8	69	10	US-09-974-300-4393
5	14.8	54.8	76	10	US-09-974-300-4374
6	14.8	54.8	76	10	US-09-974-300-4414
7	14.8	54.8	76	10	US-09-974-300-4426
8	14.8	54.8	76	10	US-09-974-300-4444
9	14.8	54.8	76	10	US-09-974-300-8409
10	14.8	54.8	76	10	US-09-974-300-8449
11	14.8	54.8	76	10	US-09-974-300-8461
12	14.8	54.8	76	10	US-09-974-300-8477
13	14.8	54.8	84	10	US-09-864-761-17329
14	14.8	54.8	87	10	US-09-864-761-19502
15	14.6	54.1	39	10	US-09-864-761-28857
16	14.4	53.3	36	10	US-09-504-231A-2483
17	14.4	53.3	36	10	US-09-504-231A-2660
18	14.4	53.3	36	10	US-09-504-231A-2816
19	14.4	53.3	36	10	US-09-274-553D-2483

C 20	14.4	53.3	36	10	US-09-274-553D-2660	Sequence 2660, Ap
C 21	14.4	53.3	36	10	US-09-274-553D-2816	Sequence 2816, Ap
C 22	14.2	52.6	36	12	US-10-078-777-8	Sequence 8, Appl
C 23	14.2	51.9	42	10	US-09-286-240-9	Sequence 353, Appl
C 24	14.1	51.9	42	10	US-09-765-272-353	Sequence 2517, Ap
C 25	13.8	51.1	36	10	US-09-504-231A-2517	Sequence 2534, Ap
C 26	13.8	51.1	36	10	US-09-504-231A-2534	Sequence 2760, Ap
C 27	13.8	51.1	36	10	US-09-504-231A-2740	Sequence 2807, Ap
C 28	13.8	51.1	36	10	US-09-504-231A-2807	Sequence 2815, Ap
C 29	13.8	51.1	36	10	US-09-504-231A-2815	Sequence 2830, Ap
C 30	13.8	51.1	36	10	US-09-504-231A-2830	Sequence 2879, Ap
C 31	13.8	51.1	36	10	US-09-504-231A-2879	Sequence 2915, Ap
C 32	13.8	51.1	36	10	US-09-274-553D-2517	Sequence 2534, Ap
C 33	13.8	51.1	36	10	US-09-274-553D-2534	Sequence 2740, Ap
C 34	13.8	51.1	36	10	US-09-274-553D-2740	Sequence 2807, Ap
C 35	13.8	51.1	36	10	US-09-274-553D-2815	Sequence 2830, Ap
C 36	13.8	51.1	36	10	US-09-274-553D-2830	Sequence 2879, Ap
C 37	13.8	51.1	36	10	US-09-274-553D-2879	Sequence 2915, Ap
C 38	13.8	51.1	36	10	US-09-864-761-26264	Sequence 1152, Ap
C 39	13.6	50.4	31	10	US-09-801-274-1152	Sequence 2090, Ap
C 40	13.6	49.6	36	10	US-09-504-231A-2090	Sequence 2279, Ap
C 41	13.4	49.6	36	10	US-09-504-231A-2279	Sequence 2515, Ap
C 42	13.4	49.6	36	10	US-09-504-231A-2515	Sequence 2709, Ap
C 43	13.4	49.6	36	10	US-09-504-231A-2709	Sequence 2830, Ap
C 44	13.4	49.6	36	10	US-09-504-231A-2830	Sequence 2879, Ap
C 45	13.4	49.6	36	10	US-09-274-553D-2090	Sequence 2664, A

ALIGNMENTS

RESULT 1
US-09-995-912-4/c
Sequence 4, Application US/09995912
Patent No. US20020137076A1
GENERAL INFORMATION:
APPLICANT: Schultz, John W.
APPLICANT: Lewis, Martin K.
TITLE OF INVENTION: RNA Polymers and Uses Thereof
FILE REFERENCE: PRNG-06684
CURRENT FILING DATE: 2001-11-28
PRIORITY FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/253,451
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-995-912-4

Query Match 81.5% Score 22; DB 10; Length 22;
Best Local Similarity 72.7% Pred. No. 0.53;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 4 GACUUGAGCCUCCAGGUCUGA 25
DB 22 GACUUGAGCCUCCAGGUCUGA 1
RESULT 2
US-09-974-300-4445
Sequence 4445, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene Expression

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FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4445
LENGTH: 67
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4445
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Query Match          54.8%; Score 14.8; DB 10; Length 67;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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Db      20 TCTGACTTTAATCAGAGGTCGAG 45
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RESULT 3
US-09-974-300-4378
Sequence 4378, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4378
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4378
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Query Match          54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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Db      20 TCTGACTTTAATCAGAGGTCGAG 45
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RESULT 4
US-09-974-300-4393
Sequence 4393, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
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NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4393
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4393
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Query Match          54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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Qy      1 UCUGACUUGAGCCUCAGGUCUGAG 26
Db      20 TCTGACTTTAATCAGAGGTCGAG 45
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RESULT 5
US-09-974-300-4374
Sequence 4374, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4374
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4374
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Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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Qy      1 UCUGACUUGAGCCUCAGGUCUGAG 26
Db      27 TCTGACTTTAATCAGAGGTCGAG 52
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RESULT 6
US-09-974-300-4414
Sequence 4414, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4414
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4414
```

Query Match	54.8%	Score 14.8	DB 10	Length 76
Best Local Similarity	50.0%	Pred. No. 8.2e+02		
Matches 13, Conservative		6, Mismatches 7	Indels 0	Gaps 0

QY 1 UCUGACUUUGAGCCUACAGGGUUCUGAG 26
 :|:|:|:|:| | | | | | | | | |
 Db 27 TCTGACTTTTATCAGAGGGGTCGAAG 52

```

RESULT 7
US-09-974-300-4426
? Sequence 4426, Application US/09974300
? Patent No. US2002014672A1
? GENERAL INFORMATION:
? APPLICANT: Berka, Randy M.
? APPLICANT: Clausen, Id Groth
? TITLE OF INVENTION: Methods For Monitoring Multiple Gene
? TITLE OF INVENTION: Expression
? FILE REFERENCE: 10085, 500-US
? CURRENT APPLICATION NUMBER: US/09/974,300
? CURRENT FILING DATE: 2001-10-05
? PRIOR APPLICATION NUMBER: 09/680,598
? PRIOR FILING DATE: 2000-10-06
? PRIOR APPLICATION NUMBER: 60/279,526
? PRIOR FILING DATE: 2001-03-27
? NUMBER OF SEQ ID NOS: 8481
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 4426
? LENGTH: 76
? TYPE: DNA
? ORGANISM: Bacillus licheniformis
US-09-974-300-4426

```

Query Match	54.88;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	50.08;	Pred. No. 8.2e+02;		
Matches	13;	Conservative	6;	Mismatches 7;
				Indels 0;
				Gaps 0.

```

QY      1 UCUGACUUUGAGCCUUCAGGGUUCUGAG 26
      :|:|:|:|:| | | | | | | |
Db     27 TCCTGACTTTTAATCAGAGGGTCGAAG 52

```

```

RESULT 8
US-09-974-300--4444
? Sequence 4444, Application US/09974300
? Patent No. US20020146721A1
? GENERAL INFORMATION:
? APPLICANT: Berkta, Randy M.
? APPLICANT: Clausen, Id Groth
? TITLE OF INVENTION: Methods For Monitoring Multiple Gene
? TITLE OF INVENTION: Expression
? FILE REFERENCE: 10085, 500-US
? CURRENT APPLICATION NUMBER: US/09/974,300
? CURRENT FILING DATE: 2001-10-05
? PRIOR APPLICATION NUMBER: 09/680,598
? PRIOR FILING DATE: 2000-10-06
? PRIOR APPLICATION NUMBER: 60/279,556
? PRIOR FILING DATE: 2001-03-27
? NUMBER OF SEQ ID NOS: 8481
? SOFTWARE: fastseqq for Windows Version 4.0
? SEQ ID NO 4444
? LENGTH: 76
? TYPE: DNA
? ORGANISM: Bacillus licheniformis
US-09-974-300-4444

```

Query Match	54.88;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	50.08;	Pred. No. 8.2e+02;		
Matches 13; Conservative	6;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1 UCUGACUUGAGACCCUACAGGUCUGAG	26		
	:-: ::: :-			

QY 1 UCUGACUUUGAGCCUCAGGUCUGAG 26
:|:|:|:|:|:| | | | | | | |

Db 27 TCTGACTTTTATCAGAGGTCGAAG 52

```

RESULT 9
US-09-974-300-8409
Sequence 8409, Application US/09974300
Patent No. US2002016731A1
GENERAL INFORMATION:
APPLICANT: Betka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085, 500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ. ID NOS: 8481
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 8409
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus clausii
US-09-974-300-8409

```

Query Match	54.8%;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	50.0%;	Pred. No. 8.2e+02;		
Matches 13; Conservative		6; Mismatches 7;	Indels 0;	Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAG 26
 ::|::|::|::|::|::|
Db 27 TCCTGACTTTTAATCAGAGGGTCGAAG 52

```

0001 10 RESULT 10
0002 US-09-974-300-8449
0003 : Sequence 8449, Application US/09974300
0004 : Patent No. US20020146721A1
0005 : GENERAL INFORMATION:
0006 : APPLICANT: Berka, Randy M.
0007 : APPLICANT: Clausen, ID Groth
0008 : TITLE OF INVENTION: Methods For Monitoring Multiple Gene
0009 : TITLE OF INVENTION: Expression
0010 : FILE REFERENCE: 10085, 500-US
0011 : CURRENT APPLICATION NUMBER: US/09/974,300
0012 : PRIORITY FILING DATE: 2001-10-05
0013 : PRIOR APPLICATION NUMBER: 09/680,598
0014 : PRIOR FILING DATE: 2000-10-06
0015 : PRIOR APPLICATION NUMBER: 60/279,526
0016 : PRIOR FILING DATE: 2001-03-27
0017 : NUMBER OF SEQ. ID NOS: 8481
0018 : SOFTWARE: FASTSEQ FOR Windows Version 4.0
0019 : SEQ. ID NO 8449
0020 : LENGTH: 76
0021 : TYPE: DNA
0022 : ORGANISM: Bacillus clausii
0023 US-09-974-300-8449

```

Query Match	54.8%;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	50.0%;	Pred. No. 8.2e+02;		
Matches 13;	Conservative	6;	Mismatches 7;	Indels 0;
			Gaps	0;

```

qy      1 ucugacuuugagccucagggucucag 26
      :|:|:|:|:| | | | | |
db     27 tctgacttttaatcagagggtcgaag 52

```

RESULT 11
US-09-974-300-8461
; Sequence 8461, Application US/09974300
; Patent No. US20020146721A1

Sequence 8461, Application US/09974300
Patent No. US20020146721A1

```

: GENERAL INFORMATION:
: APPLICANT: Berka, Randy M.
: TITLE OF INVENTION: Methods For Monitoring Multiple Gene
: TITLE OF INVENTION: Expression
: FILE REFERENCE: 10085,500-US
: CURRENT APPLICATION NUMBER: US/09/974,300
: CURRENT FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: 09/680,598
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: 60/279,526
: PRIOR FILING DATE: 2001-03-27
: NUMBER OF SEQ ID NOS: 8481
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8461
: LENGTH: 76
: TYPE: DNA
: ORGANISM: Bacillus clausii
: US-09-974-300-8461

```

Query Match	54.88;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	50.08;	Pred. No. 8.2e+02;		
Matches 13; Conservative	6;	Mismatches 7;	Indels 0;	Gaps 0

QY	1	UCUGACUUUGAGCCUCAGGGUCUGAG	26
		: : : : : : :	
Db	27	TCTGACTTTAATCAGAGGGTCGAAG	52

```

RESULT 12
US-09-974-300-8477
: Sequence 8477, Application US/09974300
: Patent No. US20020146721A1
: GENERAL INFORMATION:
: APPLICANT: Berka, Randy M.
: APPLICANT: Clausen, Ib Grolth
: TITLE OF INVENTION: Methods for Monitoring Multiple Gene
: TITLE OF INVENTION: Expression
: FILE REFERENCE: 10085 500-US
: CURRENT APPLICATION NUMBER: US/09/974,300
: CURRENT FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: 09/660,598
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: 60/279,526
: PRIOR FILING DATE: 2001-03-27
: NUMBER OF SEQ ID NOS: 8481
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8477
: LENGTH: 76
: TYPE: DNA
: ORGANISM: Bacillus clausii
: IS-09-974-300-8477

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Query Match	54.8%;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	50.0%;	Pred. No. 8.2e+02;		
Matches 13; Conservative	6;	Mismatches 7;	Indels 0;	Gaps 0

Oy 1 UCUGACUUUUGAGCCUCAGGUCUCAG 26
 :|:|:|:|:| | | | | | | |
 Db 27 TCTGACTTTTATCATCAGAGGCTCGAG 52

RESULT 13
 US-09-864-761-17329
 ; Sequence 17329, Application US/09864761
 ; Patent No. US2020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

```

1 FILE REFERENCE: Aeomica-X-1
2 CURRENT APPLICATION NUMBER: US/09/864,761
3 CURRENT FILING DATE: 2001-05-23
4 PRIOR APPLICATION NUMBER: US 60/180,312
5 PRIOR FILING DATE: 2000-02-04
6 PRIOR APPLICATION NUMBER: US 60/207,456
7 PRIOR FILING DATE: 2000-05-26
8 PRIOR APPLICATION NUMBER: US 09/632,366
9 PRIOR FILING DATE: 2000-08-03
10 PRIOR APPLICATION NUMBER: GB 24263,6
11 PRIOR FILING DATE: 2000-10-04
12 PRIOR APPLICATION NUMBER: US 60/236,359
13 PRIOR FILING DATE: 2000-09-27
14 PRIOR APPLICATION NUMBER: PCT/US01/00666
15 PRIOR FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: PCT/US01/00667
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: PCT/US01/00664
19 PRIOR FILING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/00669
21 PRIOR FILING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: PCT/US01/00665
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00668
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/00663
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/00662
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/00661
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/00670
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: US 60/234,687
35 PRIOR FILING DATE: 2000-09-21
36 PRIOR APPLICATION NUMBER: US 09/608,408
37 PRIOR FILING DATE: 2000-06-30
38 PRIOR APPLICATION NUMBER: US 09/774,203
39 PRIOR FILING DATE: 2001-01-29
40 NUMBER OF SEQ ID NOS: 49117
41 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
42 SEQ ID NO 17329

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Query Match	54.88;	Score 14.8;	DB 10;	Length 84;
Best Local Similarity	46.28;	Pred. No. 8.3e+02;		
Matches 12; Conservative	7;	Mismatches 7;	Indels 0;	Gaps 0

QY 2 CUGACUUUUGAGCCUCAGGGUCUGAGU 2
| : | : : | | : | : | : | : | :
Db 2 CTGCCCTGAACATCGGACTCTGAGT 27

RESULT 14
US-09-864-761-19502
; Sequence 19502, Application US/09864761

Query Match 54.1%; Score 14.6; DB 10; Length 79;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 5 ACUUGAGCCUCAGGGUCUGA 25
 ||: ||||| || ||: ||
 Db 50 ACTTGAGCCACAAAGCCTGA 30

Search completed: December 21, 2002, 19:28:18
 Job time : 19.0653 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 : Search time 12.7102 Seconds
(without alignments)
562.024 Million cells updates/sec

Title: US-09-121-239-26
Perfect score: 18
Sequence: 1 GAATCATCGAGCATG 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 356636 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA.*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	82.2	50	9	US-09-978-295A-294
2	14.8	82.2	50	9	US-09-978-294
3	14.8	82.2	50	9	US-09-978-182A-294
4	12.8	71.1	23	10	US-09-799-946-1
5	12.8	71.1	23	10	US-09-799-946-1
6	11.6	65.6	87	10	US-09-923-876-2188
7	11.6	64.4	89	10	US-09-864-761-23421
8	11.6	63.3	90	10	US-09-974-300-4057
9	11.2	62.2	30	10	US-09-879-257A-41
10	11.2	62.2	39	10	US-09-796-088-6
11	11.2	62.2	50	9	US-09-854-302-6
12	11.2	62.2	50	10	US-09-853-798-6
13	11.2	62.2	83	10	US-09-764-877-3299
14	11.2	62.2	87	10	US-09-764-869-2041
15	11.2	62.2	94	10	US-09-969-973-47
16	11.2	62.2	96	10	US-09-764-847-1362
17	11.2	61.1	42	10	US-09-755-633-2
18	10.8	60.0	19	9	US-09-887-880-32
19	10.8	60.0	24	9	US-09-864-921-105

20	10.8	60.0	25	9	US-09-887-880-31	Sequence 31, Appl
21	10.8	60.0	29	10	US-09-745-763-157	Sequence 157, App
22	10.8	60.0	31	10	US-09-801-274-802	Sequence 802, App
23	10.8	60.0	31	10	US-09-801-274-803	Sequence 803, App
24	10.8	60.0	35	9	US-09-993-164-19	Sequence 19, Appl
25	10.8	60.0	46	9	US-09-813-824A-7	Sequence 7, Appl1
26	10.8	60.0	73	10	US-09-783-590-2574	Sequence 2574, Ap
27	10.8	60.0	74	10	US-09-878-574-5826	Sequence 5826, Ap
28	10.8	60.0	78	10	US-09-983-965-2363	Sequence 2363, Ap
29	10.8	60.0	92	9	US-09-864-761-25377	Sequence 5, Appl1
30	10.8	60.0	92	10	US-09-864-761-25377	Sequence 25377, A
31	10.8	60.0	92	10	US-09-815-242-1251	Sequence 1251, Ap
32	10.8	60.0	92	10	US-09-815-242-1251	Sequence 1227, Ap
33	10.6	58.9	20	10	US-09-825-345-4	Sequence 4, Appl1
34	10.6	58.9	21	10	US-09-825-105-2	Sequence 2, Appl1
35	10.6	58.9	33	10	US-09-756-478-3	Sequence 3, Appl1
36	10.6	58.9	50	10	US-09-815-242-1227	Sequence 122, App
37	10.6	58.9	78	10	US-09-864-761-27282	Sequence 27282, A
38	10.6	58.9	83	10	US-09-864-761-21055	Sequence 21055, A
39	10.6	58.9	89	10	US-09-878-574-5248	Sequence 5248, Ap
40	10.6	58.9	96	10	US-09-815-343-1484	Sequence 1484, Ap
41	10.6	58.9	99	10	US-09-864-761-20823	Sequence 20823, A
42	10.6	57.8	100	10	US-09-804-599-91	Sequence 91, Appl
43	10.4	57.8	25	10	US-09-875-228-12	Sequence 12, Appl
44	10.4	57.8	35	10	US-09-875-228-12	Sequence 13638, A
45	10.4	57.8	69	10	US-09-878-574-13638	

ALIGNMENTS

RESULT 1
US-09-978-295A-294
Sequence 294, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillman, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kujo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2680PCL1
CURRENT APPLICATION NUMBER: US/09/978-295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1998-04-15

PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582

PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.28; Score 14.8; DB 9; Length 50;
 Best Local Similarity 88.98; Pred. No. 35;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGATCATCGAGCATGG 18
 Db 5 GGATCATCGATCGACGG 22

RESULT 2
 US-09-978-697-294
 Sequence 294, Application US/09978697
 Patent No. US20020169284A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C27
 CURRENT APPLICATION NUMBER: US/09/978,697
 PRIOR FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
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 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078004
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078886
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 PRIOR APPLICATION NUMBER: 60/078939
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 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
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 PRIOR FILING DATE: 1998-03-27
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 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080328
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
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PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085580
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.2% Score 14.8; DB 9; Length 50;
Best Local Similarity 88.9%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAATCATGCAGCATGG 18
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Db 5 GGAATCATGCATGCAGG 22

RESULT 3
US-09-978-192A-294
Sequence 294, Application US/09978192A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791

Mon Dec 23 08:48:02 2002

us-09-121-239-26.rnpb

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70	PRIOR APPLICATION NUMBER: 60/085704
71	PRIOR FILING DATE: 1998-05-15
72	PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.2%; Score 14.8; DB 9; Length 50;
Best Local Similarity 88.9%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 5 GAATCATCGATGCAGG 22

RESULT 4

US-09-799-946-1
; Sequence 1, Application US/09799946
; Patent No. US2002009028A1

GENERAL INFORMATION:

APPLICANT: Gudkov, Andrei
Kazarov, Alexander
Mazo, Ilya

TITLE OF INVENTION: Methods for Identifying Genetic
Suppressor Elements and Genes Associated with Malignant
Growth in Cancer Cells

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allgrettl & Witcoff, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,946
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: No. US2002009028A1man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-799-946-1

Query Match 71.1%; Score 12.8; DB 10; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 AATCATCGATGATGG 16

RESULT 5

US-09-799-946-2/c
; Sequence 2, Application US/09799946
; Patent No. US2002009028A1

GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
Kazarov, Alexander
Mazo, Ilya

TITLE OF INVENTION: Methods for Identifying Genetic
Suppressor Elements and Genes Associated with Malignant
Growth in Cancer Cells

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Allgrettl & Witcoff, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,946
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: No. US2002009028A1man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-799-946-2

Query Match 71.1%; Score 12.8; DB 10; Length 23;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCATGG 18
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DB 20 AATCATCGATGATGG 5

RESULT 6

US-09-923-876-2188/c
; Sequence 2188, Application US/09923876
; Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876
PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program


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; SEQ ID NO 2188
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyte ID No. US20020013958A1 700160195H1
US-09-923-876-2188

Query Match          65.6%; Score 11.8; DB 10; Length 87;
Best Local Similarity 86.7%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCGATG 17
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Db 79 AATCATGGCGCATG 65

RESULT 7
US-09-864-761-25421/c
; Sequence 25421, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aegm1ca-K-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25421
; LENGTH: 89
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL138970.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN HELL, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
; OTHER INFORMATION: SWISSPROT HIT: O58588, EVALUATE 3.20e+00
; OTHER INFORMATION: EST HUMAN HIT: AA724295.1, EVALUATE 7.00e-02
; OTHER INFORMATION: NR HIT: g11525786, EVALUATE 7.30e-01
US-09-864-761-25421

Query Match          64.4%; Score 11.6; DB 10; Length 89;
Best Local Similarity 77.8%; Pred. No. 2e+03; 4; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1;

QY 1 GGAATCATCGAGCGATG 18
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Db 62 GCAATATGAGGAAATG 45

RESULT 8
US-09-974-300-4057/c
; Sequence 4057, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085, 500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4057
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-4057

Query Match          63.3%; Score 11.4; DB 10; Length 90;
Best Local Similarity 92.3%; Pred. No. 2.5e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAATCATCGAGG 13
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Db 29 GTAATCATCGAGG 17

RESULT 9
US-09-879-257A-41
; Sequence 41, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIRO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBAYAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMS AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 41
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-879-257A-41

Query Match 62.2%; Score 11.2; DB 10; Length 30;
Best Local Similarity 81.2%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AATCATCGAGGCATGG 18
DB 11 ATTCAATCAAGGATATGG 26

RESULT 10
US-09-796-088-6
Sequence 6, Application US/09796088
Patent No. US20020119573A1
GENERAL INFORMATION:
APPLICANT: Shaw, Karen
APPLICANT: Kenny, Terry
APPLICANT: Shimer Jr., George H.
TITLE OF INVENTION: Footprinting Plasmid
FILE REFERENCE: 1034/0H284
CURRENT APPLICATION NUMBER: US/09/796,088
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer Sequence
US-09-796-088-6

Query Match 62.2%; Score 11.2; DB 10; Length 39;
Best Local Similarity 81.2%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATCATCGAGGCAT 16
DB 5 GAATTCCTCGAGGCAT 20

RESULT 11
US-09-854-302-6
Sequence 6, Application US/09854302
Patent No. US20020165228A1
GENERAL INFORMATION:
APPLICANT: Rydczynski, Phillip
APPLICANT: et al.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE 4H-BENZOL(1,4)OXAZIN-3-ONES
FILE REFERENCE: PM431, Patent 2.1
CURRENT APPLICATION NUMBER: US/09/854,302
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-854-302-6

Query Match 62.2%; Score 11.2; DB 9; Length 50;
Best Local Similarity 81.2%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AATCATCGAGGCATGG 18
DB 24 AATCATTTAGGCATAG 39

RESULT 12
US-09-853-798-6
Sequence 6, Application US/09853798
Patent No. US20020103193A1
GENERAL INFORMATION:
APPLICANT: Rydczynski, Phillip
APPLICANT: et al.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE 4H-BENZOL(1,4)OXAZIN-3-ONES
FILE REFERENCE: PM431, Patent 2.1
CURRENT APPLICATION NUMBER: US/09/853,798
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-853-798-6

Query Match 62.2%; Score 11.2; DB 10; Length 50;
Best Local Similarity 81.2%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AATCATCGAGGCATGG 18
DB 24 AATCATTTAGGCATAG 39

RESULT 13
US-09-764-877-3299
Sequence 3299, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3299
LENGTH: 83
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-3299

Query Match 62.2%; Score 11.2; DB 10; Length 83;
Best Local Similarity 81.2%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AATCATCGAGGCATGG 18
DB 11 AATTAGCCAGGCATGG 26

RESULT 14
US-09-764-869-2041/C
Sequence 2041, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17

; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2041
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2041

Query Match 62.2%; Score 11.2; DB 10; Length 87;
Best Local Similarity 81.2%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 AATCATCGAGCATGG 18
||| | | | | | | | |
Db 52 AATTAACCGCATGG 37

RESULT 15
US-09-969-373-47
; Sequence 47, Application US/09969373
; Patent No. US2002013852A1
; GENERAL INFORMATION:
; APPLICANT: Efferitz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 47
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-47

Query Match 62.2%; Score 11.2; DB 10; Length 94;
Best Local Similarity 81.2%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCAT 16
||| | | | | | | | |
Db 5 GGACTCATGATGATCAT 20

Search completed: December 21, 2002, 19:28:20
Job time : 14.7102 secs

Mon Dec 23 08:48:04 2002

us-09-121-239-27.rmpb

Page 1

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 : Search time 18.3592 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-27
Perfect score: 26
Sequence: 1 CACTGACCCACTGATTAACGACAG 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 356696 segs, 198428768 residues
Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_NA: *
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2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq: *
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq: *
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq: *
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq: *
6: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq: *
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq: *
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq: *
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq: *
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq: *
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: *
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	25	96.2	40	10	US-09-790-417-125
2	25	96.2	41	10	US-09-790-417-126
3	16.4	63.1	31	10	US-09-801-274-1413
4	16	61.5	88	9	US-09-909-363-17
5	15	61.5	88	9	US-09-909-363-18
6	15	57.7	22	10	US-09-790-417-127
7	15	57.7	22	10	US-09-790-417-128
8	14.4	55.4	25	10	US-09-866-108-14228
9	14.4	55.4	28	10	US-09-866-108-14229
10	14.4	55.4	28	10	US-09-766-095-12
11	14.4	55.4	28	10	US-09-766-095-12
12	14.4	55.4	28	10	US-09-766-095-12
13	14.4	55.4	28	10	US-09-766-095-12
14	14.4	55.4	28	10	US-09-766-095-12
15	14.4	55.4	28	10	US-09-766-095-12
16	14.4	55.4	28	10	US-09-766-095-12
17	13.4	51.5	25	10	US-09-864-761-23997
18	13.4	51.5	25	10	US-09-864-761-27487
19	13.2	50.8	36	10	US-09-866-108-14230

20	13	50.0	90	10	US-09-753-436-47	Sequence 47, Appl
21	13	50.0	98	9	US-09-924-400-282	Sequence 282, Appl
22	13	50.0	98	10	US-09-810-936-282	Sequence 282, Appl
23	13	50.0	98	10	US-09-429-755-282	Sequence 282, Appl
24	12.8	49.2	21	10	US-09-853-386-145	Sequence 145, Appl
25	12.8	48.5	69	10	US-09-775-743A-10	Sequence 10, Appl
26	12.6	48.5	26	10	US-09-911-935A-17	Sequence 17, Appl
27	12.6	48.5	78	10	US-09-374-671-56	Sequence 56, Appl
28	12.4	47.7	25	10	US-09-866-108-14226	Sequence 14226, A
29	12.4	47.7	25	10	US-09-866-108-14231	Sequence 14231, A
30	12.4	47.7	28	10	US-09-812-216-8	Sequence 8, Appl
31	12.4	47.7	51	10	US-09-917-265-96	Sequence 96, Appl
32	12.4	47.7	78	10	US-09-777-564-1563	Sequence 1563, Appl
33	12.4	47.7	78	10	US-09-983-965-3131	Sequence 3131, Appl
34	12.4	47.7	79	10	US-09-783-590-1166	Sequence 1166, Appl
35	12.4	47.7	92	10	US-09-864-761-31467	Sequence 31467, A
36	12.4	47.7	100	10	US-09-728-446-1353	Sequence 1353, Appl
37	12.2	46.9	45	9	US-09-905-291A-337	Sequence 337, Appl
38	12.2	46.9	45	10	US-09-903-320B-337	Sequence 337, Appl
39	12.2	46.9	45	10	US-09-903-088B-337	Sequence 337, Appl
40	12.2	46.9	79	9	US-09-870-753-75	Sequence 75, Appl
41	12.2	46.9	84	10	US-09-864-761-17357	Sequence 17357, A
42	12.2	46.9	88	10	US-09-864-761-26014	Sequence 26014, A
43	12	46.2	20	9	US-09-966-955A-17	Sequence 17, Appl
44	12	46.2	23	10	US-09-910-635-2	Sequence 2, Appl
45	12	46.2	23	10	US-09-956-412-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-790-417-125/c
Sequence 125 Application US/09790417
Patent No US20010031470A1
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT FILING DATE: 2001-02-22
PRIORITY FILING DATE: 1999-07-21
PRIORITY FILING DATE: 1998-03-13
PRIORITY FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 125
LENGTH: 40
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: native bcr
US-09-790-417-125
Query Match 96.2% Score 25; DB 10; Length 40;
Best Local Similarity 100.0%; Prod. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ACTGACCCACTGATTAACGACAG 26
DB 40 ACTGACCCACTGATTAACGACAG 16

RESULT 2

US-09-790-417-126/c
; Sequence 126, Application US/09790417
; Patent No. US20010031470A1
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W.
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: bcr/abl translocation
US-09-790-417-126

Query Match

Best Local Similarity 96.2%; Score 25; DB 10; Length 41;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTGAGCCACTGATTTAAGCAGAG 26
|||||

Db 41 ACTGAGCCACTGATTTAAGCAGAG 17

RESULT 3

US-09-801-274-1413
; Sequence 1413, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825,2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1413

Query Match 63.1%; Score 16.4; DB 10; Length 31;
Best Local Similarity 85.0%; Pred. No. 47;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCCACTGATTTAAGCAGAG 26
|||||

Db 2 GCCACTGATTTAAGCAGAG 21

RESULT 4

US-09-909-363-17
; Sequence 17, Application US/09909363
; Patent No. US20020164783A1
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew
; TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
; AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMB
; AAV VECTORS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,363
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/171,759
; FILING DATE: 20-OCT-1998
; APPLICATION NUMBER: PCT/US98/21937
; FILING DATE: 20-OCT-1998
; APPLICATION NUMBER: 08/955,400
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: 60/108,162
; FILING DATE: 21-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 226272003802
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-909-363-17

Query Match

Best Local Similarity 61.5%; Score 16; DB 9; Length 88;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTCAGCCACTGATTTAAGCAGAG 26
|||||

Db 43 CCCACCCCTGATTTAAGCAGAG 66

RESULT 5

US-09-909-363-18/c
; Sequence 18, Application US/09909363
; Patent No. US20020164783A1
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew

TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMBINANT
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/909,363
APPLICATION NUMBER: 19-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,759
FILING DATE: 20-OCT-1998
APPLICATION NUMBER: PCT/US98/21937
FILING DATE: 20-OCT-1998
APPLICATION NUMBER: 08/955,400
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: 60/108,162
FILING DATE: 21-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Caterline M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 226272003802
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-909-363-18
Query Match 61.5%; Score 16; DB 9; Length 88;
Best Local Similarity 79.2%; Pred. No. 93;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CTCAGCCACTGATTTAAGCAGAG 26
DB 50 CCCACCCCTGTATATACAGAG 27
RESULT 6
US-09-790-417-127
Sequence 127, Application US/09790417
Patent No. US20010031470A1
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection

FILE REFERENCE: PRO-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/790,417
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 127
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: probe for native bcr
US-09-790-417-127
Query Match 57.7%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TGGATTTAAGCAGAG 26
DB 1 TGGATTTAAGCAGAG 15
RESULT 7
US-09-790-417-128
Sequence 128, Application US/09790417
Patent No. US20010031470A1
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: PRO-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/790,417
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 128
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: probe for bcr/abl translocation
US-09-790-417-128
Query Match 57.7%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TGGATTTAAGCAGAG 26
DB 1 TGGATTTAAGCAGAG 15
RESULT 8
US-09-866-108-14228
Sequence 14228, Application US/09866108

Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 14228
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-14228

Query Match 55.4%; Score 14.4; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

3 CTCAGCCACTGGATTAAAGAGAG 26
2 CTCAGCCCCAGATTAACGAGAG 25

RESULT 9
US-09-866-108-14229
Sequence 14229, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 14229
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-14229

Query Match 55.4%; Score 14.4; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

3 CTCAGCCACTGGATTAAAGAGAG 26
1 CTCAGCCCCAGATTAACGAGAG 24

RESULT 10
US-09-766-095-12/C
Sequence 12, Application US/09766095
Patent No. US20020062016A1
GENERAL INFORMATION:
APPLICANT: Sheriol H. McDonough, Thomas B. Ryder,
Yuesing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
OLIGONUCLEOTIDES AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 50x or 55sx
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)

Mon Dec 23 08:48:04 2002

us-09-121-239-27.rnpb

Page 5

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 26-Jan-01
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837
FILING DATE: 10-Jul-90
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-766-095-12
Query Match 55.4%; Score 14.4; DB 10; Length 28;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGATTAAGCAG 24
Db 28 CCCTCAGATCTGCATATTAAGCAG 5

RESULT 11
US-09-766-095-64
Sequence 64, Application US/09766095
Patent No. US20020062016A1
GENERAL INFORMATION:
APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
Yeasting Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
OLIGONUCLEOTIDES AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (version 3.30)
SOFTWARE: Wordperfect (version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 26-Jan-01
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837
FILING DATE: 10-Jul-90
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
NAME: Warburg, Richard J.
```

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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-766-095-64
Query Match 55.4%; Score 14.4; DB 10; Length 28;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGATTAAGCAG 24
Db 1 CCCTCAGATCTGCATATTAAGCAG 24

RESULT 12
US-09-766-095-78/C
Sequence 78, Application US/09766095
Patent No. US20020062016A1
GENERAL INFORMATION:
APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
Yeasting Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
OLIGONUCLEOTIDES AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (version 3.30)
SOFTWARE: Wordperfect (version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 26-Jan-01
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837
FILING DATE: 10-Jul-90
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
NAME: Warburg, Richard J.
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US-09-766-095-78

Query Match 55.4%; Score 14.4; DB 10; Length 28;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACTCAGCCACTGGATTAGACG 24
1 ||||| ||||| ||||| ||||| |||||
Db 28 CCTCAGATCCTGCATATAGACG 5

RESULT 13

US-09-766-095-92
Sequence 92, Application US/09766095
Patent No. US20020062016A1

GENERAL INFORMATION:

APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,

Yeastang Yang

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: Wordperfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766.095

FILING DATE: 18-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/013,406

FILING DATE: 26-JAN-01

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837

FILING DATE: 10-Jul-90

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 196/189

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 92:

US-09-766-095-92

Query Match 55.4%; Score 14.4; DB 10; Length 28;

Best Local Similarity 58.3%; Pred. No. 4.1e+02;

Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACTCAGCCACTGGATTAGACG 24

1 ||||| ||||| ||||| ||||| |||||

Db 1 CCTCAGATCCTGCATATAGACG 24

RESULT 14

US-09-991-003B-19/c

Sequence 19, Application US/09991003B

Patent No. US20020177125A1

GENERAL INFORMATION:

APPLICANT: KAMB, Carl Alexander

APPLICANT: KAMITZ, Mark Aaron

APPLICANT: TENG, David Heng-Fai

TITLE OF INVENTION: Human Rhinovirus Assays, and Compositions Therefrom

FILE REFERENCE: 29345/36971A

CURRENT APPLICATION NUMBER: US/09/991,003B

CURRENT FILING DATE: 2002-11-16

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.0

SEQ ID NO 19

LENGTH: 42

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: rh2B.F1 primer

US-09-991-003B-19

Query Match 55.4%; Score 14.4; DB 9; Length 42;

Best Local Similarity 93.8%; Pred. No. 4.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CACTCAGCCACTGGAT 16

1 ||||| ||||| ||||| ||||| |||||

Db 26 CACTCAGCCCTGGAT 11

RESULT 15

US-09-864-761-23997

Sequence 23997, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aeomla-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23997
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC022392.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EST_HUMAN HIT: AW861102.1, EVALU 9.50e-01
US-09-864-761-23997

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Query Match          55.4%; Score 14.4; DB 10; Length 80;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 2 ACTCAGCCACTGATTTAAGCAGA 25
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Db 3 ATTATCCATGATGATTTATCAGA 26

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Search completed: December 21, 2002, 19:28:21
 Job time : 19:3592 secs

